STIC Search Report
Biotech-Chem Library

USPTO

TO: Phillip Gambel
Location: cm1/9e12
Art Unit: 1644
Friday, October 03, 2003

Case Serial Number: 09758173

From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Gambel,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

RUSH

09/758173

sira
Search and Information
Resources Administration

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                GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October 2, 2003, 13:10:05 ; Search time 76.372 Seconds
                                        (without alignments)
                                        8304.972 Million cell updates/sec

Title:          US-09-758-173-7
Perfect score:  1437
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:     1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1177.8	82.0	19040	4	US-09-343-485A-3	Sequence 3, Appli
4	1155.8	80.4	1576	1	US-08-157-101A-6	Sequence 6, Appli
5	1142	79.5	1350	1	US-08-157-101A-9	Sequence 9, Appli
6	1131.8	78.6	1617	2	US-08-378-939-9	Sequence 9, Appli
7	1127.4	78.5	9209	1	US-08-149-099C-3	Sequence 3, Appli
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ALIGNMENTS

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; Sequence 7, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/487,550
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
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;   STRANDEDNESS: not relevant
;   TOPOLOGY: linear
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;   NAME/KEY: mat_peptide
;   LOCATION: 1..1437
US-08-487-550-7

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Best Local Similarity 100.0%; Pred. No. 0;
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GenCore version 5.1.6
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Run on: October 2, 2003, 19:53:01 ; Search time 284.274 seconds
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Title: US-09-758-173-7
Perfect score: 1437
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Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

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SUMMARIES

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5	1216	100.0	1437	13	US-10-073-138-4	Sequence 4, Appli
6	1216	84.6	1616	10	US-09-822-830A-572	Sequence 572, App
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20	1141.4	79.4	1356	10	US-09-822-698A-27	Sequence 27, Appl
21	1141.4	79.4	1431	10	US-09-225-108A-15	Sequence 15, Appl
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41	1127.4	78.5	18986	11	US-10-203-754A-40	Sequence 40, Appl
42	1127	78.4	1428	12	US-09-825-012-10	Sequence 10, Appl
43	1120.6	78.0	1404	10	US-09-726-258-68	Sequence 68, Appl
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-948-429B-7
; Sequence 7, Application US/09948429B
; Patent No. US2002017689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRSPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/948,429B
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021

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    LENGTH:  1437 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  not relevant
    TOPOLOGY:  linear
  MOLECULE TYPE:  peptide
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  1..1437
  FEATURE:
    NAME/KEY:  mat_peptide
    LOCATION:  1..1437
US-09-948-429B-7
```

```
Query Match            100.0%;  Score 1437;  DB 10;  Length 1437;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1437;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 ATGGGTTGAGCCTCATCTGCTCTTCCTTGTCGCGTGTTGCTACGCGTGTCCAGTGTGAG     60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGGTTGAGCCTCATCTGCTCTTCCTTGTCGCGTGTTGCTACGCGTGTCCAGTGTGAG     60

Qy     61 GTGCAACTGGTGAGTCTCTGGGGAGGCTTGGTCCAGCCTGGGCGGTCCCTGAGAGTCTCC    120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGCAACTGGTGAGTCTCTGGGGAGGCTTGGTCCAGCCTGGGCGGTCCCTGAGAGTCTCC    120

Qy    121 TGTGCAGTCTCTGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA    180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTGCAGTCTCTGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA    180

Qy    181 GGGAAGGGGCCGGAATGGGTAGGTTCATTAGAAACAAACCGAACGGTGGGACAACAGAA    240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGAAGGGGCCGGAATGGGTAGGTTCATTAGAAACAAACCGAACGGTGGGACAACAGAA    240

Qy    241 TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATGATTCAAAAGCATCGCC   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATGATTCAAAAGCATCGCC   300

Qy    301 TATCTGCAAATGAGCAGCCTGAAAATGAGGACACGGCCGTCTTATTACTGTACTACATCC   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TATCTGCAAATGAGCAGCCTGAAAATGAGGACACGGCCGTCTTATTACTGTACTACATCC   360

Qy    361 TACATTCACATTGTCGGGGTGGTTGTCTGTCTATGGAGGTTACTTCGAATTCTGGGCCAG   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TACATTCACATTGTCGGGGTGGTTGTCTGTCTATGGAGGTTACTTCGAATTCTGGGCCAG   420

Qy    421 GGCGCCCTGCTGTCACCGTCTCCTCAGCTAGCACCACCAAGGGCCCATCGGTCTTCCCCCTGGCA   480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCGCCCTGCTGTCACCGTCTCCTCAGCTAGCACCACCAAGGGCCCATCGGTCTTCCCCCTGGCA   480

Qy    481 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC   540

Qy    541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC   600

Qy    601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC   660

Qy    661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC   720

Qy    721 AAGGTGGACAAGAAAGCAGAGCCCAAATCTGTGACAAAACTCACACATGCCCACCGTGC    780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGGTGGACAAGAAAGCAGAGCCCAAATCTGTGACAAAACTCACACATGCCCACCGTGC    780

Qy    781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC    840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC    840

Qy    841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA    900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA    900

Qy    901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA    960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA    960

Qy    961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG   1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG   1020

Qy   1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA   1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA   1080

Qy   1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTAC   1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGAACCCACAGGTGTAC   1140

Qy   1141 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC   1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGTC   1200

Qy   1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC   1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC   1260

Qy   1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG   1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG   1320

Qy   1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTTCTCATGCTCCGTGATGCAT   1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTTCTCATGCTCCGTGATGCAT   1380

Qy   1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA     1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA     1437
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RESULT 2
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US-10-124-807-7
; Sequence 7, Application US/10124807
; Publication No. US20030166207A1
GENERAL INFORMATION:
  APPLICANT:  Anderson, Darrell R.
  TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
  TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
  TITLE OF INVENTION:  PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
  TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
  NUMBER OF SEQUENCES:  12
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
    STREET:  699 Prince Street
    CITY:  Alexandria
    STATE:  VA
    COUNTRY:  USA
    ZIP:  22314
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/10/124,807
    FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  09/383,916
    FILING DATE:
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              GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:   October  2, 2003, 08:56:23  ; Search time 56.0907 seconds
                                        (without alignments)
                                        1352.654 Million cell updates/sec

Title:           US-09-758-173-8
Perfect score:   2561
Sequence:        1 MGWSLLLFLVAVATRVQCE........MHEALHNHYTQKSLSLSPGK 478

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:  1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2561	100.0	478	19	AAW63763	Macaque primatized
2	2561	100.0	478	23	AAU11644	Protein sequence o
3	2555	99.8	478	18	AAW01820	Primatised anti-hu
4	2205	86.1	468	24	ABP58275	Humanised 3D6 anti
5	2197	85.8	461	14	AAR42162	Anti-HIV-1 recombi
6	2184.5	85.3	452	20	AAY29458	Recombinant immuno
7	2184.5	85.3	452	21	AAB30322	Humanised anti-IL-
8	2184.5	85.3	452	21	AAY77766	Humanised anti-IL-
9	2184.5	85.3	452	24	ABU59512	Humanised Mouse an
10	2184.5	85.3	452	24	ABU13799	Humanised mouse an
11	2183	85.2	474	23	AAO14065	Heavy chain protei
12	2183	85.2	474	24	ABU08017	Human monoclonal r
13	2180.5	85.1	449	23	AAO18400	Mature humanised m
14	2177.5	85.0	477	23	AAU14288	Human novel protei
15	2176	85.0	470	24	ABB81109	Anti-tissue factor
16	2176	85.0	470	23	ABP72748	Anti-tissue factor
17	2175.5	84.9	447	24	AAE33522	Human AQC2 heavy c
18	2175.5	84.9	452	19	AAW69316	Anti-IL-8 humanise
19	2172.5	84.8	475	13	AAR20057	Heavy chain of 3D6
20	2169.5	84.7	447	24	AAE33523	Human AQC2 heavy c
21	2169.5	84.7	461	22	AAU07745	Humanised monoclon
22	2165.5	84.6	447	24	AAE33524	Human AQC2 heavy c
23	2162	84.4	470	13	AAR22757	Reshaped CAMPATH-1
24	2161.5	84.4	444	21	AAY32263	Humanised anti-CD2
25	2160	84.3	449	24	ABP58273	Humanised 3D6 anti
26	2160	84.3	451	22	AAE12715	Human recombinant
27	2160	84.3	451	24	ABO58807	Mucin 1 (MUC-1) bi
28	2156.5	84.2	481	13	AAR24442	Sequence of antibo
29	2156	84.2	476	23	ABB81110	Anti-VEGF heavy ch
30	2154	84.1	449	21	AAY68810	A rat heavy chain
31	2151	84.0	477	15	AAR47453	chiT84.12 H3 heavy
32	2149.5	83.9	731	22	AAM52156	Humanised HMFG-1 h
33	2149.5	83.9	741	22	AAM52159	Humanised HMFG-1 h
34	2148	83.9	470	22	AAE27923	Human C2B8 antibod
35	2148	83.9	470	24	ABB82832	Antibody C2B8 heav
36	2147	83.8	464	23	ABG91842	Human antibody fra
37	2147	83.8	464	22	ABG78151	Human Fv molecule
38	2144.5	83.7	729	22	AAM52158	Humanised HMFG-1 h
39	2144.5	83.7	739	22	AAM52161	Humanised HMFG-1 h
40	2140	83.6	582	22	AAB81987	Ganglioside GD3 sp
41	2139	83.6	470	21	AAB08026	A dimeric anti-CD2
42	2138.5	83.5	459	14	AAR42066	Human anti-HBs hea
43	2138.5	83.5	730	22	AAM52157	Humanised HMFG-1 h
44	2138.5	83.5	740	22	AAM52160	Humanised HMFG-1 h
45	2137.5	83.5	444	24	AAB34876	BIWA4/8 antibody h

ALIGNMENTS

```
RESULT 1
AAW63763
ID   AAW63763 standard; Protein; 478 AA.
XX
AC   AAW63763;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 7B6 heavy chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9919706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;  97WO-US19906.
XX
PR   08-NOV-1996;  96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brans P,  Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35487.
```

```
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 4b; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 7B6 heavy
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   MAb's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence  478 AA;

Query Match             100.0%;  Score 2561;  DB 19;  Length 478;
Best Local Similarity   100.0%;  Pred. No. 4.2e-152;
Matches   478;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120

Qy  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180

Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240

Qy  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300

Qy  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360

Qy  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420

Qy  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478

RESULT 2
AAU11644
ID   AAU11644 standard; Protein; 478 AA.
XX
AC   AAU11644;
XX
DT   12-MAR-2002  (first entry)
```

```
XX
DE   Protein sequence of primatised form of the heavy chain of 7B6 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; mutein.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,   Hanna N,   Brams P;
XX
DR   WPI; 2002-089895/12.
DR   N-PSDB; AAS17245.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 4b; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present protein
CC   sequence represents the heavy chain of 7B6, a primatised antibody
CC   used in the invention to induce apoptosis.
XX
SQ   Sequence  478 AA;

Query Match             100.0%;  Score 2561;  DB 23;  Length 478;
Best Local Similarity   100.0%;  Pred. No. 4.2e-152;
Matches   478;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120

Qy  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
```

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  2, 2003, 09:07:34 ; Search time 21.0061 seconds
                                         (without alignments)
                                         2188.349 Million cell updates/sec

Title:         US-09-758-173-8
Perfect score: 2561
Sequence:    1 MGWSLILLFLVAVATRVQCE.........MHEALHNHYTQKSLSLSPGK 478
Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:    283308 seqs, 95168682 residues

Total number of hits satisfying chosen parameters:   283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_76:*
             1: pir1:*
             2: pir2:*
             3: pir3:*
             4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1763	68.8	330	1	GHHU	Ig gamma-1 chain C
2	1626.5	63.5	377	2	A23511	Ig gamma-3 chain C
3	1624.5	63.4	377	2	A60764	Ig gamma-3 chain C
4	1600	62.5	326	1	G2HU	Ig gamma-2 chain C
5	1586.5	61.9	327	1	G4HU	Ig gamma-4 chain C
6	1494.5	58.4	444	2	PC4436	monoclonal antibod
7	1478	57.7	470	2	S22080	Ig heavy chain pre
8	1467.5	57.3	469	2	S37483	Ig gamma-2a chain
9	1429	55.8	472	2	S31459	Ig gamma-1 chain -
10	1415	55.3	374	2	S69339	Ig heavy chain V r
11	1415	55.3	446	2	S40295	Ig gamma-2a chain
12	1392	54.4	474	1	G2MS11	Ig gamma-2b chain
13	1338.5	52.3	475	2	S01321	Ig gamma-2b chain
14	1259	49.2	328	2	I47159	Ig gamma-2a chain
15	1256	49.0	255	4	S31866	Ig gamma-1 chain C
16	1253	48.9	328	2	I47160	Ig gamma-2b chain
17	1250	48.8	234	2	PT0207	Ig gamma chain C r
18	1227	47.9	328	1	I47158	Ig gamma 1 chain C
19	1226.5	47.9	323	1	GHRB	Ig gamma chain C r
20	1223	47.8	328	2	I47161	Ig gamma 3 chain C
21	1212.5	47.3	329	1	G2GP	Ig gamma-2 chain C
22	1157.5	45.1	308	2	C30554	Ig heavy chain C r
23	1152	45.0	289	1	G3HUWI	Ig gamma-3 heavy c
24	1148	44.8	326	2	PS0017	Ig gamma-1 chain C
25	1142.5	44.6	333	2	PS0018	Ig gamma-2b chain C
26	1138	44.4	324	1	G1MS	Ig gamma-1 chain C
27	1137	44.4	329	1	G3MSC	Ig gamma-3 chain C
28	1133	44.2	393	1	G1MSM	Ig gamma-1 chain C
29	1126	44.0	398	1	G3MSM	Ig gamma-3 chain C
30	1122	43.8	330	1	G2MSA	Ig gamma-2a chain
31	1119.5	43.7	335	1	G2MSAB	Ig gamma-2a chain
32	1117	43.6	399	1	G2MSAM	Ig gamma-2a chain
33	1114.5	43.5	329	2	S00847	Ig gamma-2c chain
34	1108	43.3	322	2	PS0019	Ig gamma-2a chain
35	1088.5	42.5	327	2	S06611	Ig gamma-2 chain C
36	1080	42.2	405	2	G2MSBM	Ig gamma-2b chain
37	1062	41.5	277	2	I47162	Ig gamma 4 chain C
38	1009	39.4	548	2	S38864	Ig epsilon chain C
39	863.5	33.7	549	2	S04845	Ig heavy chain pre
40	829.5	32.4	249	2	S69340	Ig heavy chain VHI
41	797.5	31.1	572	2	B46529	Ig Y heavy chain (
42	797	31.1	220	2	A49444	Ig gamma-1 heavy c
43	771	30.1	627	2	S14683	Ig mu chain precur
44	758.5	29.6	241	2	S69131	Ig heavy chain (DO
45	739	28.9	218	2	A36040	Ig heavy chain V-I

ALIGNMENTS

```
RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:217370
A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:217370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:217370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96; 'R',98-135 <CUN>
A;Note: this sequence has the Glm(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',155-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni
```

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igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunoglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the Glm(3) and Glm(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A95565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match             68.8%;  Score 1763;  DB 1;  Length 330;
Best Local Similarity   99.7%;  Pred. No. 3e-97;
Matches   329;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   149  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS   60

Qy   209  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG  268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG  120

Qy   269  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN  328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN  180

Qy   329  STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE  388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE  240

Qy   389  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  300

Qy   449  QQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
          ||||||||||||||||||||||||||||||
Db   301  QQGNVFSCSVMHEALHNHYTQKSLSLSPGK  330
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RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene.
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Genetics:
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match             63.5%;  Score 1626.5;  DB 2;  Length 377;
Best Local Similarity   81.7%;  Pred. No. 4.1e-89;
Matches   308;  Conservative   10;  Mismatches   12;  Indels   47;  Gaps    1;

Qy   149  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  208
          |||||||||||||  ::|||||||||||||||||||||||||||||||||||||||||||
Db     1  ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS   60

Qy   209  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA----------------------  246
          ||||||||||||||||||||| ||||||||||||||
Db    61  GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC  120

Qy   247  ---------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT  281
                                     ||||  ||||||||||||||||||||||||||
Db   121  DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT  180

Qy   282  LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH  341
          |||||||||||||||||||||||||||||||:||||||||||||||::||||||||||||
Db   181  LMISRTPEVTCVVVDVSHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH  240

Qy   342  QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK  401
          ||||||||||||||||||||||||||||:||||||||||||||||::|:|||||||||||
Db   241  QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK  300

Qy   402  GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE  461
          ||||||||||||| |||||||| |||| ||||||||||||||||||||||||:|||||||
Db   301  GFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE  360

Qy   462  ALHNHYTQKSLSLSPGK  478
          |||| ||||||||||||
Db   361  ALHNRFTQKSLSLSPGK  377
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RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (GmbO, b1, c3, c5, u) with an IGHG4 conv
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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                    GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on:    October  2, 2003, 08:56:23  ; Search time 13.1847 Seconds
                                        (without alignments)
                                        1704.917 Million cell updates/sec

Title:        US-09-758-173-8
Perfect score:  2561
Sequence:   1 MGWSLILLFLVAVATRVQCE........MHEALHNHYTQKSLSLSPGK 478

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:    127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:    127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database:    SwissProt_41:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

            %
Result      Query
No.   Score Match Length DB  ID              Description
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  1   1763  68.8   330   1   GC1_HUMAN       P01857 homo sapien
  2   1600  62.5   326   1   GC2_HUMAN       P01859 homo sapien
  3   1586.5 61.9  327   1   GC4_HUMAN       P01861 homo sapien
  4   1226.5 47.9  323   1   GC_RABIT        P01870 oryctolagus
  5   1212.5 47.3  329   1   GC2_CAVPO       P01862 cavia porce
  6   1157  45.2   290   1   GC3_HUMAN       P01860 homo sapien
  7   1148  44.8   326   1   GC1_RAT         P20759 rattus norv
  8   1142.5 44.6  333   1   GCB_RAT         P20761 rattus norv
  9   1138  44.4   324   1   GC1_MOUSE       P01868 mus musculu
 10   1137  44.4   329   1   GC3_MOUSE       P22436 mus musculu
 11   1133  44.2   393   1   GC1M_MOUSE      P01869 mus musculu
 12   1126  44.0   398   1   GC3M_MOUSE      P03987 mus musculu
 13   1122  43.8   330   1   GCAA_MOUSE      P01863 mus musculu
 14   1119.5 43.7  335   1   GCAB_MOUSE      P01865 mus musculu
 15   1117  43.6   399   1   GCAM_MOUSE      P20762 rattus norv
 16   1114.5 43.5  329   1   GCC_RAT         P20760 rattus norv
 17   1108  43.3   322   1   GCA_RAT         P01866 mus musculu
 18   1085  42.4   336   1   GCB_MOUSE       P01867 mus musculu
 19   1080  42.2   405   1   GCBM_MOUSE      P01854 homo sapien
 20    489  19.1   428   1   EPC_HUMAN       P01855 rattus norv
 21    483.5 18.9   429   1   EPC_RAT         P06336 mus musculu
 22    465  18.2   421   1   EPC_MOUSE       P01872 mus musculu
 23    448  17.5   455   1   MUC_MOUSE       P01805 rattus norv
 24    442  17.3   142   1   HV01_RAT        P01871 homo sapien
 25    442  17.3   454   1   MUC_HUMAN       P01873 mus musculu
 26    438  17.1   476   1   MUCM_MOUSE      P03988 oryctolagus
 27    437  17.1   458   1   MUC_RABIT       P01795 mus musculu
 28    430  16.8   144   1   HV26_MOUSE      P04221 oryctolagus
 29    427  16.7   479   1   MUCM_RABIT      P20768 suncus muri
 30    425  16.6   457   1   MUC_SUNMU       P01874 canis famil
 31    420  16.4   450   1   MUC_CANFA       P01787 mus musculu
 32    419  16.4   123   1   HV18_RAT        P01789 mus musculu
 33    418.5 16.3   122   1   HV20_MOUSE
 34    418   16.3   123   1   HV19_MOUSE      P01788 mus musculu
 35    416.5 16.3   122   1   HV21_MOUSE      P01790 mus musculu
 36    416   16.2   117   1   HV17_MOUSE      P01786 mus musculu
 37    415.5 16.2   454   1   MUC_MESAU       P06337 mesocricetu
 38    415   16.0   123   1   HV22_MOUSE      P01791 mus musculu
 39    410   16.0   123   1   HV23_MOUSE      P01792 mus musculu
 40    403   15.7   391   1   MUCB_HUMAN      P04220 homo sapien
 41    399   15.6   123   1   HV25_HUMAN      P01794 mus musculu
 42    397   15.5   117   1   HV3C_HUMAN      P01764 homo sapien
 43    397   15.5   123   1   HV24_MOUSE      P01793 mus musculu
 44    396   15.5   115   1   HV32_MOUSE      P01801 mus musculu
 45    394   15.4   438   1   HVCS_HETFR      P23087 heterodontu

                                             ALIGNMENTS

RESULT 1
GC1_HUMAN
ID   GC1_HUMAN      STANDARD;      PRT;    330 AA.
AC   P01857;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-1 chain C region.
GN   IGHG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82274238; PubMed=6287432;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [3]
RP   SEQUENCE OF 136-329 (EU).
RX   MEDLINE=71064025; PubMed=5530842;
RA   Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA   Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL   Biochemistry 9:3171-3181(1970).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN NIE).
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [5]
RP   SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
```

Additional alignment reference entries:
```
RP   SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [2]
RL   Nucleic Acids Res. 10:4071-4079(1982).
RT   "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RA   Ellison J.W., Berson B.J., Hood L.E.;
RX   MEDLINE=82274238; PubMed=6287432;
RP   SEQUENCE FROM N.A.
RN   [1]
```

```
RT   Intrachain disulfide bonds";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1991).
CC   -!- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
CC       G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
CC       MARKER & THE G1M (NON-1) MARKERS.
CC   -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC       35,116,198,269 & 272.
CC   -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC       155,166,177,195,198,269, AND 272 AND IN THE ORDER OF RESIDUES
CC       268-272.
CC   -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC       RESIDUES 198,267&272.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use  by non-profit institutions as  long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GIHU.
DR   PDB; 1FC1; 15-JUL-92.
DR   PDB; 1FC2; 15-JUL-92.
DR   PDB; 1AJ7; 12-NOV-97.
DR   PDB; 1D5B; 09-FEB-00.
DR   PDB; 1D5I; 09-FEB-00.
DR   PDB; 1D6V; 04-OCT-00.
DR   PDB; 1DN2; 17-MAY-00.
DR   PDB; 1E4K; 06-JUN-01.
DR   PDB; 1FCC; 20-JUL-95.
DR   PDB; 1H2H; 12-JUN-02.
DR   PDB; 1I7Z; 08-AUG-01.
DR   PDB; 1IIS; 16-MAY-01.
DR   PDB; 1IIX; 16-MAY-01.
DR   PDB; 1L6X; 10-APR-02.
DR   PDB; 2RCS; 12-NOV-97.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100;
DR   GO; GO:0005524; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       INTERCHAIN (WITH LIGHT CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    144    204
FT   CARBOHYD    250    308       N-LINKED (GLCNAC...).
FT   MOD_RES     180    180       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT     330    330       K -> R (IN G1M(3) MARKER).
FT                               /FTId=VAR_003886.
FT   VARIANT      97     97       D -> E (IN G1M(NON-1) MARKER).
FT                               /FTId=VAR_003887.
FT   VARIANT     239    239       L -> M (IN G1M(NON-1) MARKER).
FT                               /FTId=VAR_003888.
FT   VARIANT     241    241
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    147
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    166
FT   TURN        168    171
FT   STRAND      176    179
FT   TURN        180    181
FT   STRAND      182    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      260    265
FT   STRAND      270    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      305    312
FT   TURN        313    314
FT   TURN        316    317
FT   STRAND      320    325
SQ   SEQUENCE   330 AA;  36106 MW;  3770EE106C2FA33D CRC64;

Query Match             68.8%;  Score 1763;  DB 1;  Length 330;
Best Local Similarity   99.7%;  Pred. No. 1.2e-117;
Matches  329;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   0;

Qy    149 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy    209 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 268
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db     61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy    269 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy    329 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy    389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
```

```
                    GenCore version 5.1.6
             Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October 2, 2003, 08:56:23 ; Search time 46.2581 Seconds
                                        (without alignments)
                                        2666.544 Million cell updates/sec

Title:       US-09-758-173-8
Perfect score: 2561
Sequence:    1 MGWSLILLFLVAVATRVQCE........MHEALHNHYTQKSLSLSPGK 478

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:    830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:    830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_23:*
              1:  sp_archea:*
              2:  sp_bacteria:*
              3:  sp_fungi:*
              4:  sp_human:*
              5:  sp_invertebrate:*
              6:  sp_mammal:*
              7:  sp_mhc:*
              8:  sp_organelle:*
              9:  sp_phage:*
             10:  sp_plant:*
             11:  sp_rodent:*
             12:  sp_virus:*
             13:  sp_vertebrate:*
             14:  sp_unclassified:*
             15:  sp_rvirus:*
             16:  sp_bacterial:*
             17:  sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2178.5	85.1	471	4	Q8TC77	Q8tc77 homo sapien
2	2103.5	82.1	521	4	Q8N4Y9	Q8n4y9 homo sapien
3	1838	71.8	473	4	Q8TC63	Q8tc63 homo sapien
4	1632.5	63.7	469	11	Q8R3V9	Q8r3v9 mus musculu
5	1612.5	63.0	509	4	Q8NF17	Q8nf17 homo sapien
6	1495.5	58.4	473	11	Q9D8L4	Q9d8l4 mus musculu
7	1480.5	57.8	473	11	Q91Z05	Q91z05 mus musculu
8	1480	57.8	468	11	Q99L31	Q99l31 mus musculu
9	1472.5	57.5	473	11	Q99L25	Q99l25 mus musculu
10	1469.5	57.4	437	11	Q9R1A4	Q9r1a4 mus musculu
11	1458.5	57.0	463	11	Q99LC4	Q99lc4 mus musculu
12	1415	55.3	474	11	Q8R3H6	Q8r3h6 mus musculu
13	1268	49.5	701	6	Q96PQ8	Q96pq8 homo sapien
14	1262.5	49.3	337	6	Q95M34	Q95m34 equus cabal
15	879.5	34.3	597	6	Q96BB9	Q96bb9 homo sapien
16	845.5	33.0	499	4	Q8N5K4	Q8n5k4 homo sapien
17	845	33.0	613	4	Q8WUK1	Q8wuk1 homo sapien
18	805	31.4	494	4	Q96K68	Q96k68 homo sapien
19	792	30.9	484	11	Q8VEA0	Q8vea0 mus musculu
20	789.5	30.8	614	4	Q96GA6	Q96ga6 homo sapien
21	789	30.8	278	11	Q921K1	Q921k1 mus musculu
22	786.5	30.7	487	11	Q99KA4	Q99ka4 mus musculu
23	775.5	30.3	493	4	Q8NCL6	Q8ncl6 homo sapien
24	769.5	30.0	479	11	Q91WP5	Q91wp5 mus musculu
25	760	29.7	486	11	Q91Z07	Q91z07 mus musculu
26	731	28.5	613	11	Q8VCX7	Q8vcx7 mus musculu
27	727.5	28.4	480	11	Q91XEl	Q91xel mus musculu
28	719	28.1	500	4	Q9BRV0	Q9brv0 homo sapien
29	716.5	28.0	597	4	Q9BU10	Q9bu10 homo sapien
30	714.5	27.9	597	11	Q9BQB8	Q9bqb8 homo sapien
31	712	27.8	482	11	Q8K172	Q8k172 mus musculu
32	712	27.8	496	4	Q96DK0	Q96dk0 homo sapien
33	710.5	27.7	481	11	Q91WT1	Q91wt1 mus musculu
34	710.5	27.7	497	4	Q8WY24	Q8wy24 homo sapien
35	708	27.6	613	4	Q96EY0	Q96ey0 homo sapien
36	706.5	27.6	588	4	Q8WUX4	Q8wux4 homo sapien
37	706.5	27.6	618	4	Q96AA6	Q96aa6 homo sapien
38	700	27.3	488	11	Q8K0F2	Q8k0f2 mus musculu
39	687	26.8	488	11	Q91WR1	Q91wr1 mus musculu
40	684	26.7	480	11	Q8K0Z4	Q8k0z4 mus musculu
41	671.5	26.2	481	11	Q8VCV5	Q8vcv5 mus musculu
42	670.5	26.2	489	11	Q8VCX4	Q8vcx4 mus musculu
43	669	26.1	484	11	Q99LA6	Q99la6 mus musculu
44	666.5	26.0	481	11	Q91WT3	Q91wt3 mus musculu
45	650.5	25.4	482	11	Q91X92	Q91x92 mus musculu

ALIGNMENTS

```
RESULT 1
Q8TC77
ID   Q8TC77            PRELIMINARY;     PRT;    471 AA.
AC   Q8TC77;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024289; AAH24289.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE  471 AA;  51791 MW;  388F7F4CF588660E CRC64;

Query Match       85.1%;   Score 2178.5;  DB 4;  Length 471;
Best Local Similarity  87.2%;  Pred. No. 1.4e-180;
Matches 416;  Conservative 15;  Mismatches 27;  Indels 19;  Gaps 3;

Qy   8  LFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWV  67
        :|||: ||||||||||||||||| :|||| ||| :| ||||||| :||||||||||||||
Db   8  VFLVAILEGVQCEVQLVESGGGLVKPGGGLRLSCAASGFTFSSYSMNWVRQAPGKGLEWV  67

Qy  68  GFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCT----TSY  121
        |||:|| || |||||||| :||||||||:| : |||| ||| :||||||||    ||:
Db  68  SSMSS--SSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSY  125
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Qy  122  ISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF  181
Db  126  ------WFDLWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF  174
Qy  182  PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK  241
Db  175  PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK  234
Qy  242  VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED  301
Db  235  VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED  294
Qy  302  PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCCKVSNKALPA  361
Db  295  PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCCKVSNKALPA  354
Qy  362  PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN  421
Db  355  PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN  414
Qy  422  YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
Db  415  YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  471
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```
RESULT 2
Q8N4Y9
ID   Q8N4Y9    PRELIMINARY;    PRT;    521 AA.
AC   Q8N4Y9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells from Tonsils;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033178; AAH33178.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 3.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   521 AA;   57156 MW;   2AC7D22E7D6CAA2 CRC64;

Query Match             82.1%;  Score 2103.5;  DB 4;  Length 521;
Best Local Similarity   76.4%;  Pred. No. 5.1e-174;
Matches  401;  Conservative  27;  Mismatches  42;  Indels  55;  Gaps  3;

Qy    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP   60
Db    5  LSWVLLVVFLQG---VQCEVQLVDSGGGLVQPGGSLRLSCAASGFIVSDHYVEWVRQAP   60
Qy   61  GKGPEWVGFIRNKPNGGTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120
Db   61  GKGPEWVGCFRSKAHKSTEYAASVKGRFTILRDDSKNSVHLQMNSLKTDDTAVYYC---  117
Qy  121  YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180
Db  118  -VRDLEGAGKYDWYFDIWGRGILVTVSSASTKGPSVFPLAPCSRSTSGGTAALGCLVKDY  176
Qy  181  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240
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Db  177  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNT  236
Qy  241  KVDKKA------EPKSCDK  253
Db  237  KVDKRVELKTPLGDTHTCPRCPEPKSCDTPPCPRCPEPKSCDT  296
Qy  254  THTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDSHEDPEVKFNWYVDGV  313
Db  297  PPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDSHEDPEVQFKWYVDGV  356
Qy  314  EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCCKVSNKALPAPIEKTISKAKGQ  373
Db  357  EVFNAKTKPREEQFNSTFRVVSVLTVLHQDWLNGKEYKCCKVSNKALPAPIEKTISKTKGQ  416
Qy  374  PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG  433
Db  417  PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDG  476
Qy  434  SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
Db  477  SFFLYSKLTVDKSRWQQGNIFSCSVMHEALNRFTQKSLSLSPGK  521
```

```
RESULT 3
Q8TC63
ID   Q8TC63    PRELIMINARY;    PRT;    473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;   51986 MW;   E29920B09BA369F5 CRC64;

Query Match             71.8%;  Score 1838;  DB 4;  Length 473;
Best Local Similarity   75.5%;  Pred. No. 5.1e-151;
Matches  357;  Conservative  33;  Mismatches  67;  Indels  16;  Gaps  4;

Qy    8  LFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSG--FTFSDHYMYWFRQAPGKGPE   65
Db   15  LLIVAAPRWVLSRLQLQESGPGLLKPSVTLSLTCTVSGDSVASSSYWGWVRQPPGKGLE   74
Qy   66  WVGFIRNKPNGGTEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTSYISHC  125
Db   75  WIGTIN--FSGNMYYSPSLRSVTMSADMSENSFYLKLDSVTAADTAVYYCAAGHL--  128
Qy  126  RGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPV  185
Db  129  -----VMGFGAHWGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV  183
Qy  186  TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK  245
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                 GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      October  2, 2003, 09:12:09  ; Search time 21.2295 Seconds
                                           (without alignments)
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Title:       US-09-758-173-8
Perfect score:  2561
Sequence:    1 MGWSLILLFLVAVATRVQCE.........MHEALHNHYTQKSLSLSPGK 478

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:     328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                           SUMMARIES
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3	2184.5	85.3	452	3	US-09-027-449-71	Sequence 71, Appl
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5	2184.5	85.3	452	4	US-09-121-952A-71	Sequence 71, Appl
6	2184.5	85.3	452	4	US-09-234-340A-71	Sequence 71, Appl
7	2146.5	83.8	449	4	US-09-679-397-2	Sequence 2, Appli
8	2146.5	83.8	449	4	US-09-680-148-2	Sequence 2, Appli
9	2146.5	83.8	449	4	US-09-304-465A-2	Sequence 2, Appli
10	2138.5	83.5	459	1	US-09-157-101A-7	Sequence 7, Appli
11	2135	83.4	451	3	US-08-887-352B-18	Sequence 18, Appl
12	2135	83.4	451	3	US-09-109-207C-18	Sequence 18, Appl
13	2135	83.4	451	3	US-09-282-505-2	Sequence 2, Appli
14	2135	83.4	451	3	US-09-054-255-2	Sequence 2, Appli
15	2135	83.4	451	3	US-09-296-005-18	Sequence 18, Appl
16	2135	83.4	451	4	US-09-282-846-2	Sequence 2, Appli
17	2135	83.4	451	4	US-09-680-145-2	Sequence 2, Appli
18	2132	83.2	451	2	US-08-887-352B-14	Sequence 14, Appli
19	2132	83.2	451	2	US-08-887-352B-16	Sequence 16, Appl
20	2132	83.2	451	3	US-09-466-151-65	Sequence 65, Appl
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23	2132	83.2	451	3	US-09-296-005-14	Sequence 14, Appl
24	2132	83.2	451	3	US-09-296-005-16	Sequence 16, Appl
25	2132	83.2	453	4	US-08-466-151-8	Sequence 8, Appli
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27	2100	82.0	476	2	US-08-378-939-10	Sequence 10, Appl
28	2089.5	81.6	467	3	US-09-049-672A-8	Sequence 8, Appli
29	2078	81.1	472	4	US-08-793-450-8	Sequence 8, Appli
30	2073.5	81.0	475	2	US-09-740-002-25	Sequence 25, Appl
31	2073	80.9	476	3	US-08-487-555-4	Sequence 4, Appli
32	2073	80.9	476	4	US-09-526-099-4	Sequence 4, Appli
33	2071.5	80.9	475	2	US-09-740-002-27	Sequence 27, Appl
34	2069	80.8	449	1	US-08-458-516-13	Sequence 13, Appl
35	2064	80.6	472	4	US-09-301-593-43	Sequence 43, Appl
36	2058.5	80.4	467	1	US-08-704-744-81	Sequence 81, Appl
37	2056.5	80.3	446	3	US-08-397-411-7	Sequence 7, Appli
38	2054	80.2	468	4	US-09-485-737B-67	Sequence 67, Appl
39	2054	80.2	472	4	US-09-301-593-30	Sequence 30, Appl
40	2054	80.2	711	4	US-09-485-737B-90	Sequence 90, Appl
41	2053	80.2	476	4	US-08-487-550-12	Sequence 12, Appl
42	2053	80.2	476	3	US-09-526-098-12	Sequence 12, Appl
43	2046.5	79.9	473	3	US-09-049-672A-4	Sequence 4, Appli
44	2040.5	79.7	552	3	PCT-US93-07832-23	Sequence 23, Appl
45	2037.5	79.6	469	2	US-07-934-373C-23	Sequence 23, Appl

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                           ALIGNMENTS

RESULT 1
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; Sequence 8, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION:   TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION:   PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION:   IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES:  12
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/487,550
;    FILING DATE: 07-JUN-1995
;    CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
;    TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO:  8:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 478 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-487-550-8

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Best Local Similarity 100.0%;  Pred. No. 1.2e-198;
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US-09-526-098-8

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  Matches  478;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
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; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
;     APPLICANT: Gonzalez, Tania R.
;     APPLICANT: Leong, Steven R.
;     APPLICANT: Presta, Leonard G.
;     TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
;     TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
;     NUMBER OF SEQUENCES: 72
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Genentech, Inc.
;        STREET: 1 DNA Way
;        CITY: South San Francisco
;        STATE: California
;        COUNTRY: USA
;        ZIP: 94080
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/09/027,449
;        FILING DATE: 20-Feb-1998
;        CLASSIFICATION: 435
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: 60/074,330
;        FILING DATE: 22-Jan-1998
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: 60/038,664
;        FILING DATE: 21-Feb-1997
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; Sequence 8, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
;     APPLICANT: Anderson, Darrell R.
;     TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;     TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;     TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;     TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;     NUMBER OF SEQUENCES: 12
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;        STREET: 699 Prince Street
;        CITY: Alexandria
;        STATE: VA
;        COUNTRY: USA
;        ZIP: 22314
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/09/526,098
;        FILING DATE:
;        CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: 09/383,916
;        FILING DATE:
;        APPLICATION NUMBER: US 08/487,550
;        FILING DATE: 07-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Teskin, Robin L.
;        REGISTRATION NUMBER: 35,030
;        REFERENCE/DOCKET NUMBER: 012712-131
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 703-836-6620
;        TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 478 amino acids
;        TYPE: amino acid
;        TOPOLOGY: linear
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              GenCore version 5.1.6
         Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on:    October  2, 2003, 09:18:44  ; Search time 179.446 Seconds
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Title:            US-09-758-173-8
Perfect score:    2561
Sequence:         1 MGWSLILLFLVAVATRVQCE........MHEALHNHYTQKSLSLSPGK 478

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Total number of hits satisfying chosen parameters:    587654

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2561	100.0	478	10	US-09-948-429B-8	Sequence 8, Appli
2	2561	100.0	478	12	US-10-124-807-8	Sequence 8, Appli
3	2561	100.0	478	12	US-10-291-532-8	Sequence 8, Appli
4	2561	100.0	478	14	US-10-124-905-8	Sequence 8, Appli
5	2184.5	85.3	452	11	US-09-726-258-71	Sequence 71, Appl
6	2183	85.2	474	12	US-10-225-108A-3	Sequence 3, Appli
7	2183	85.2	474	12	US-09-848-832-3	Sequence 3, Appli
8	2176	85.0	470	15	US-10-020-786-9	Sequence 9, Appli
9	2176	85.0	470	15	US-10-227-694-5	Sequence 5, Appli
10	2160	84.3	451	10	US-09-822-698A-26	Sequence 26, Appl
11	2156	84.2	476	15	US-10-020-786-11	Sequence 11, Appl
12	2154	84.1	449	10	US-09-736-371B-21	Sequence 21, Appl
13	2149.5	83.9	731	10	US-09-825-012-46	Sequence 46, Appl
14	2149.5	83.8	741	10	US-09-825-012-55	Sequence 55, Appl
15	2146.5	83.8	449	12	US-10-356-974-2	Sequence 2, Appli
16	2146.5	83.8	449	15	US-10-253-366-2	Sequence 2, Appli
17	2146.5	83.8	449	15	US-10-316-694-2	Sequence 2, Appli
18	2144.5	83.7	729	10	US-09-825-012-52	Sequence 52, Appl
19	2144.5	83.7	739	10	US-09-825-012-61	Sequence 61, Appl
20	2138.5	83.5	730	10	US-09-825-012-49	Sequence 49, Appl
21	2138.5	83.5	740	10	US-09-825-012-58	Sequence 58, Appl
22	2137.5	83.5	444	15	US-10-150-475A-6	Sequence 6, Appli
23	2135	83.4	451	12	US-09-920-171-18	Sequence 18, Appl
24	2135	83.4	451	12	US-10-113-996-18	Sequence 18, Appl
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36	2129	83.1	453	11	US-09-925-179-8	Sequence 8, Appli
37	2129	83.1	451	12	US-09-925-179-66	Sequence 66, Appl
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39	2124	82.9	470	15	US-10-216-484-147	Sequence 147, App
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41	2123	82.9	470	15	US-10-216-484-145	Sequence 145, App
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45	2118	82.7	470	12	US-10-384-933-117	Sequence 117, App

ALIGNMENTS

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RESULT 1
US-09-948-429B-8
; Sequence 8, Application US/09948429B
Patent No. US2002017689A1
GENERAL INFORMATION:
     APPLICANT: Anderson, Darrell R.
     TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
     TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
     TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
     TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
     NUMBER OF SEQUENCES: 12
     CORRESPONDENCE ADDRESS:
        ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
        STREET:     699 Prince Street
        CITY:       Alexandria
        STATE:      VA
        COUNTRY:    USA
        ZIP:        22314
     COMPUTER READABLE FORM:
        MEDIUM TYPE:       Floppy disk
        COMPUTER:          IBM PC compatible
        OPERATING SYSTEM:  PC-DOS/MS-DOS
        SOFTWARE:          PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
        APPLICATION NUMBER:  US/09/948,429B
        FILING DATE:
        CLASSIFICATION:
     PRIOR APPLICATION DATA:
        APPLICATION NUMBER:  09/383,916
        FILING DATE:
        APPLICATION NUMBER:  US 08/487,550
        FILING DATE:         07-JUN-1995
     ATTORNEY/AGENT INFORMATION:
        NAME:  Teskin, Robin L.
        REGISTRATION NUMBER:  35,030
        REFERENCE/DOCKET NUMBER:  012712-131
     TELECOMMUNICATION INFORMATION:
        TELEPHONE:  703-836-6620
```

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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-429B-8

Query Match     100.0%;   Score 2561;  DB 10;  Length 478;
Best Local Similarity  100.0%;  Pred. No. 1.2e-169;
Matches 478;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
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Db    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
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Db   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120

Qy  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180

Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
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Qy  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
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Qy  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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Db  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478

RESULT 2
US-10-124-807-8
; Sequence 8, Application US/10124807
; Publication No. US20030166207A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
FILING DATE:
CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-124-807-8

Query Match     100.0%;   Score 2561;  DB 12;  Length 478;
Best Local Similarity  100.0%;  Pred. No. 1.2e-169;
Matches 478;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120

Qy  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180

Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
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Qy  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
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Db  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300

Qy  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
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Db  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360

Qy  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
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Qy  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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RESULT 3
US-10-291-532-8
; Sequence 8, Application US/10291532
; Publication No. US20030180290A1
GENERAL INFORMATION:
APPLICANT: HARIHARAN, KANDASAMY
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
FILE REFERENCE: 037003/291872
CURRENT APPLICATION NUMBER: US/10/291,532
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/331,187
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 09/758,173
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OM nucleic - nucleic search, using sw model

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Run on: October 2, 2003, 13:01:50 ; Search time 1867.6 Seconds
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Title: US-09-758-173-9
Perfect score: 711
Sequence: 1 ATGAGGGTCCCGCCTCAGCT........CCCCTACAGAATGTTCATGA 711

Scoring table: IDENTITY_NUC
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Searched: 2888711 seqs, 2454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

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       13: gb_un:*
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       31: em_htg_inv:*
       32: em_htg_other:*
       33: em_htg_mus:*
       34: em_htg_pln:*
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       37: em_htg_vrt:*
       38: em_sy:*
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       40: em_htgo_mus:*
       41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	711	100.0	711	6	AR108866	AR108866 Sequence
2	711	100.0	711	6	AR265200	AR265200 Sequence
3	711	100.0	711	6	BD063038	BD063038 Identific
4	582.6	81.9	935	6	AR135362	AR135362 Sequence
5	575.4	80.9	790	9	AB064208	AB064208 Homo sapi
6	573	80.6	870	6	BD176841	BD176841 A.method
7	573	80.6	870	9	HSIGLV	X14583 Human mRNA
8	571.2	80.3	903	9	BC020233	BC020233 Homo sapi
9	570.6	80.3	827	9	AB064143	AB064143 Homo sapi
10	566.6	79.7	800	9	AB064188	AB064188 Homo sapi
11	566.4	79.7	919	9	BC022098	BC022098 Homo sapi
12	556	79.6	815	9	AB064149	AB064149 Homo sapi
13	562.8	79.2	812	9	AB064148	AB064148 Homo sapi
14	562.8	79.2	816	9	AB064147	AB064147 Homo sapi
15	562.4	79.1	827	9	AB064219	AB064219 Homo sapi
16	562.2	79.1	750	9	HSIGVL027	X57817 Human rearr
17	560	78.8	747	9	HSIGVL006	X57806 Human rearr
18	558	78.5	821	9	AB064141	AB064141 Homo sapi
19	558	78.5	824	9	AB064227	AB064227 Homo sapi
20	557.6	78.4	804	9	AB064172	AB064172 Homo sapi
21	556.4	78.3	790	9	AB064206	AB064206 Homo sapi
22	556.4	78.3	824	9	AB064226	AB064226 Homo sapi
23	555.4	78.1	827	9	HSIGVL021	X57811 Human rearr
24	554.8	78.0	816	9	AB064150	AB064150 Homo sapi
25	554.4	78.0	790	9	AB064169	AB064169 Homo sapi
26	554.4	78.0	803	9	AB064166	AB064166 Homo sapi
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ALIGNMENTS

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LOCUS   AR108866   711 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION   Sequence 9 from patent US 6113898.
ACCESSION   AR108866
VERSION   AR108866.1 GI:12825142
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 711)
  AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
  TITLE   Human B7.1-specific primatized antibodies and transfectomas
             expressing said antibodies
  JOURNAL   Patent: US 6113898-A 9 05-SEP-2000;

Pred. No. is the number of results predicted by chance to have a

Left column

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Best Local Similarity 100.0%;  Pred. No. 5.8e-174;
Matches  711;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
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Qy   181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACACATTAACAAGCGACCCTCAGGAATTTCT 240
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Db   181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACACATTAACAAGCGACCCTCAGGAATTTCT 240

Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCCTCCCATCACTGGGCTCCAG 300
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Qy   361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
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Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480
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Qy   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
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Db   661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711


RESULT 2
LOCUS       AR265200     711 bp   DNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6492134.
ACCESSION   AR265200
VERSION     AR265200.1  GI:29693621
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 711)
  AUTHORS   Aquin,S. and Vezina,Louis.-P.
  TITLE     Method for producing polyhydroxyalkanoates in recombinant organisms
  JOURNAL   Patent: US 6492134-A 9 10-DEC-2002;
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Right column

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FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT   160 a   226 c   193 g   132 t
ORIGIN

Query Match          100.0%;  Score 711;  DB 6;  Length 711;
Best Local Similarity 100.0%;  Pred. No. 5.8e-174;
Matches  711;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 ATGAGGGTCCCGCTCAGCTCCTGGGCTCCTGCTGCTCCCAGGTGCACGATGT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGAGGGTCCCGCTCAGCTCCTGGGCTCCTGCTGCTCCCAGGTGCACGATGT 60

Qy    61 GAGTCTGTCCTGACACAGCCGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GAGTCGTGTCCTGACACAGCCGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120

Qy   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
         |||||||||||||||||||||||||||||  ||||  |||||  |||||||||||||||
Db   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180

Qy   181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT 240
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Db   181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT 240

Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCCTCCCATCACTGGGCTCCAG 300
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Db   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGTA 360

Qy   361 TTCGGACGAGGGGACCCGCCTCCTCTAGTCAGCCGCAAGGCTGCCCCCTCGGTCACT 420
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Db   361 TTCGGAGGAGGGGACCCGCCTCCTCTAGTCAGCCGCAAGGCTGCCCCCTCGGTCACT 420

Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480
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Db   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480

Qy   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
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Db   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540

Qy   541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC 600
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Qy   661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711
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Db   661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711


RESULT 3
LOCUS       BD063038     711 bp   DNA    linear   PAT 27-AUG-2002
DEFINITION  Identification of unique binding interactions between certain
            antibodies and the human B7.1 and B7.2 co-stimulatory antigens.
ACCESSION   BD063038
VERSION     BD063038.1  GI:22608641
KEYWORDS    JP 2001504693-A/5.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 711)
  AUTHORS   Anderson,D.R., Hanna,N., Brams,P. and Hard,C.
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```
                    GenCore version 5.1.6
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        October  2, 2003, 12:12:30 ; Search time 145.625 seconds
                                            (without alignments)
                                            13179.730 Million cell updates/sec

Title:         US-09-758-173-9
Perfect score: 711
Sequence:      1 ATGAGGGTCCCGCCTCAGCT........CCCCTACAGAATGTTCATGA 711

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:      5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  N_Geneseq_19Jun03:*
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       23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
       24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
       25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	711	100.0	711	19	AAV35488	Macaque primatized
2	711	100.0	711	24	AAS17246	DNA sequence of a
3	709.4	99.8	711	18	AAT62512	Primatised anti-hu
4	582.6	81.9	935	22	AAC66525	Human immune syste
5	573	80.6	870	24	AAL50812	Human cancer statu
6	571.4	80.4	884	11	AAQ03609	Sequence encoding
7	565.2	79.5	762	22	AAC84209	Plasmid Glambda-1B
8	558.8	78.6	5679	22	AAC84207	Plasmid Glambda-1A

```
    9 | 552.6 | 77.7 | 768 | 20 | AAX06953 | Monoclonal antibod
c  10 | 552.6 | 77.7 | 768 | 20 | AAX06954 | Monoclonal antibod
   11 | 547  | 76.9 | 654 | 14 | AAQ49835 | Anti-HIV-1 recombi
   12 | 546.2 | 76.8 | 810 | 23 | AAS87270 | DNA encoding novel
   13 | 545.6 | 76.7 | 9532 | 25 | ABZ37360 | MALIA3 nucleotide
   14 | 540.2 | 76.0 | 705 | 19 | AAT62509 | Primatised anti-hu
   15 | 540.2 | 76.0 | 705 | 19 | AAV35484 | Macaque primatized
   16 | 540.2 | 76.0 | 705 | 24 | AAS17242 | DNA sequence of a
   17 | 534.8 | 75.2 | 2112 | 24 | ABQ75369 | Human lung specifi
   18 | 533.2 | 75.0 | 651 | 19 | AAV11293 | Antibody HB4C5 lig
   19 | 533.2 | 75.0 | 708 | 22 | AAH47902 | Human type antihum
   20 | 532.2 | 74.9 | 915 | 24 | ABN97248 | Gene #3746 used to
   21 | 532.2 | 74.9 | 915 | 24 | ABK64815 | Human benign prost
   22 | 532.2 | 74.9 | 915 | 24 | ABL65478 | Lung cancer relate
   23 | 532.2 | 74.9 | 964 | 24 | ABQ93374 | Human cDNA SEQ ID
   24 | 530.2 | 74.6 | 895 | 22 | AAC66530 | Human immune syste
   25 | 527.6 | 74.2 | 705 | 25 | ABX15392 | Human IgG anti-rhe
   26 | 523.6 | 73.6 | 708 | 22 | AAH47904 | Human type antihum
   27 | 522.8 | 73.5 | 1845 | 24 | ABL49526 | Plasmid scFv(CCO46
   28 | 518.8 | 73.0 | 708 | 22 | AAH47898 | Human type antihum
   29 | 510.6 | 71.8 | 891 | 22 | AAC66528 | Human immune syste
   30 | 509.2 | 71.6 | 763 | 22 | AAS83480 | DNA encoding novel
   31 | 502.6 | 70.7 | 902 | 14 | AAQ35100 | Antibody D lambda
   32 | 499.4 | 70.2 | 889 | 23 | AAS77073 | DNA encoding novel
   33 | 498.6 | 70.1 | 906 | 22 | AAK51914 | Human polynucleoti
   34 | 496.4 | 69.8 | 951 | 23 | AAS90539 | DNA encoding novel
   35 | 494.4 | 69.5 | 783 | 23 | AAS83483 | DNA encoding novel
   36 | 494.4 | 69.5 | 876 | 23 | AAS83478 | DNA encoding novel
   37 | 493.8 | 69.5 | 888 | 21 | AAA95786 | Human immune syste
c  38 | 487.4 | 68.6 | 1636 | 23 | ABV22585 | Human prostate exp
c  39 | 487.4 | 68.6 | 1636 | 23 | ABV28405 | Human prostate exp
   40 | 486.6 | 68.4 | 756 | 23 | AAS83477 | DNA encoding novel
   41 | 484.2 | 68.1 | 885 | 19 | AAV34321 | Human secreted pro
   42 | 484.2 | 68.1 | 885 | 24 | AAD44672 | Human secreted pro
   43 | 484.2 | 68.1 | 885 | 24 | AAD44890 | Human secreted pro
   44 | 484.2 | 68.1 | 885 | 25 | ABX97002 | Human secreted pro
   45 | 482.8 | 67.9 | 702 | 24 | ABS67760 | DNA encoding antib
```

ALIGNMENTS

```
RESULT 1
AAV35488
ID   AAV35488 standard; DNA; 711 BP.
XX
AC   AAV35488;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 16C10 light chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..711
FT                  /*tag=     a
FT                  /product= 16C10 light chain
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;  97WO-US19906.
XX
PR   08-NOV-1996;  96US-0746361.
XX
```

```
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63764.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 5a; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 16C10 light chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAB's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;

Query Match            100.0%;   Score 711;  DB 19;   Length 711;
Best Local Similarity  100.0%;   Pred. No. 9.9e-172;
Matches  711;  Conservative   0;  Mismatches   0;   Indels   0;   Gaps   0;

Qy     1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCCTGCTCCTCGCTCCCAGGTGCACGATGT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCCTGCTCCTCGCTCCCAGGTGCACGATGT 60

Qy    61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120

Qy   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180

Qy   181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACAATAACAAGCGACCCTCAGGAATTCT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACAATAACAAGCGACCCTCAGGAATTCT 240

Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCTCGGCCATCACTGGGCTCCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCTCGGCCATCACTGGGCTCCAG 300

Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360

Qy   361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGTCACCCCCTCGGTCACT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGTCACCCCCTCGGTCACT 420

Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480

Qy   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540

Qy   541 GCGGGAGTGGGAGACCACCACCACCCTCCAACAACAAGCAACAACAAGTACGCGGCCAGCAGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCGGGAGTGGGAGACCACCACCACCCTCCAACAACAAGCAACAACAAGTACGCGGCCAGCAGC 600

Qy   601 TACCTGAGCCTGACGCCTGAGCGGTGGGAGTCCACAGAAGTCCACAGAAGCTACAGCTGCCAGGTCACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TACCTGAGCCTGACGCCTGAGCGGTGGGAGTCCACAGAAGTCCACAGAAGCTACAGCTGCCAGGTCACG 660

Qy   661 CATGAAGGAGGACACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCATGA 711
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CATGAAGGAGGACACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCATGA 711
```

```
RESULT 2
AAS17246
ID   AAS17246 standard; DNA; 711 BP.
XX
AC   AAS17246;
XX
DT   12-MAR-2002  (first entry)
XX
DE   DNA sequence of a primatised form of the light chain of 16C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..711
FT                   /*tag= a
FT                   /product= "Light chain of 16C10 antibody"
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Hanna N,  Brams P;
XX
DR   WPI; 2002-089895/12.
DR   P-PSDB; AA011645.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   useful for treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 5a; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
```

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2003  Compugen Ltd.

QM nucleic - nucleic search, using sw model

Run on:        October  2, 2003, 13:05:20 ; Search time 1175.83 Seconds
                                            (without alignments)
                                            14696.420 Million cell updates/sec

Title:         US-09-758-173-9
Perfect score: 711
Sequence:      1 ATGAGGGTCCCGCTCAGCT.........CCCCTACAGAATGTTCATGA 711

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters:      45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
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            2:   em_esthum:*
            3:   em_estin:*
            4:   em_estmu:*
            5:   em_estov:*
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           11:   gb_htc:*
           12:   gb_est3:*
           13:   gb_est4:*
           14:   gb_est5:*
           15:   em_estfun:*
           16:   em_estom:*
           17:   em_gss_hum:*
           18:   em_gss_inv:*
           19:   em_gss_pln:*
           20:   em_gss_vrt:*
           21:   em_gss_fun:*
           22:   em_gss_mam:*
           23:   em_gss_mus:*
           24:   em_gss_pro:*
           25:   em_gss_rod:*
           26:   em_gss_phg:*
           27:   em_gss_vrl:*
           28:   gb_gss1:*
           29:   gb_gss2:*

                    SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Result No.	% Score	Match	Query Length	DB	ID	Description
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2	562.6	79.1	913	13	BQ708635	BQ708635 AGENCOURT
3	559	78.6	894	13	BQ708570	BQ708570 AGENCOURT
4	558.6	78.6	819	10	BG685644	BG685644 602637629

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                                                             ALIGNMENTS

  5   557.8  78.5  873  13  BQ712653  BQ712653  AGENCOURT
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  7   555.2  78.1  755  12  BG755185  BG755185  602714114
  8   552.2  77.7  687  14  CB554445  CB554445  MMSP0066_
  9   552.2  77.7  1007 12  BM920020  BM920020  AGENCOURT
 10   551.6  77.6  1060 12  BM906351  BM906351  AGENCOURT
 11   551.6  77.6  910  10  BG757147  BG757147  602710516
 12   549.4  77.3  857  13  BQ890529  BQ890529  AGENCOURT
 13   549    77.2  764  10  BG755548  BG755548  602716230
 14   545    76.8  817  12  BI835917  BI835917  603085650
 15   545.4  76.7  896  10  BG685967  BG685967  602638530
 16   544.8  76.6  823  10  BG686957  BG686957  602650951
 17   544.6  76.6  849  10  BG756887  BG756887  602710380
 18   544.6  76.6  1124 12  BM918688  BM918688  AGENCOURT
 19   541.8  76.2  900  10  BF663927  BF663927  601145588
 20   541.6  76.2  936  13  BQ709123  BQ709123  AGENCOURT
 21   539.8  75.9  832  12  BI819072  BI819072  603003425
 22   539    75.8  774  10  BG398461  BG398461  602439745
 23   538.4  75.7  948  10  BG757977  BG757977  602715021
 24   538.4  75.7  870  10  BG684025  BG684025  602635632
 25   538.2  75.7  873  10  BG686011  BG686011  602638561
 26   537.4  75.6  935  10  BG755314  BG755314  602714059
 27   537    75.5  868  10  BG745909  BG745909  602724089   c
 28   535.6  75.3  701  10  BG398176  BG398176  602440022
 29   535.4  75.3  626  13  BU787530  BU787530  io34g05.x
 30   535.4  75.3  947  12  BI819216  BI819216  603034633
 31   532.2  74.9  864  10  BG758242  BG758242  602712422
 32   532.2  74.9  902  10  BQ883560  BQ883560  AGENCOURT
 33   529.8  74.5  792  12  BG760202  BG760202  602733508
 34   529.6  74.5  813  10  BG755102  BG755102  602711415
 35   529.4  74.4  783  12  BM007830  BM007830  603617507
 36   527    74.1  894  13  BQ709510  BQ709510  AGENCOURT
 37   524    73.7  784  14  CB956723  CB956723  AGENCOURT
 38   521.8  73.4  957  13  BX446259  BX446259  BX446259
 39   521.8  73.4  1150 13  BX449367  BX449367  BX449367
 40   521.4  73.3  1201 13  BX462166  BX462166  BX462166
 41   519.8  73.1  911  10  BG398014  BG398014  602439543
 42   519.6  73.1  767  12  BI836367  BI836367  603083069
 43   519    73.0  695  12  BM831144  BM831144  K-EST0104
 44   519    73.0  1201 13  BX442894  BX442894  BX442894
 45   518.6  72.9  945  13  BX446252  BX446252  BX446252


RESULT 1
BQ711292
LOCUS       BQ711292     AGENCOURT_8353826 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278335
                         956 bp    mRNA    linear    EST 16-JUL-2002
DEFINITION  5', mRNA sequence.
ACCESSION   BQ711292
VERSION     BQ711292.1   GI:21850191
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 956)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2466  row: c  column: 08
            High quality sequence start: 10
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BQ708635
LOCUS       BQ708635                 913 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8351417 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282312
            5', mRNA sequence.
ACCESSION   BQ708635
VERSION     BQ708635.1  GI:21847534
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2476 row: i  column: 01
            High quality sequence stop: 663.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6282312"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life technologies). Note: this is a
                     NIH_MGC Library."
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Qy    124 TGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCT   180
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                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life technologies). Note: this is a
                     NIH_MGC Library."
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Best Local Similarity   88.6%;  Pred. No. 4.5e-130;
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                    Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on:    October 2, 2003, 13:10:05  ; Search time 37.7874 Seconds
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Perfect score:   711
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Scoring table:   IDENTITY_NUC
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Total number of hits satisfying chosen parameters:     1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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ALIGNMENTS

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; Sequence 9, Application US/0487550
; Patent No. 6113898
GENERAL INFORMATION:
   APPLICANT: Anderson, Darrell R.
   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
   NUMBER OF SEQUENCES: 12
   CORRESPONDENCE ADDRESS:
     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
     STREET: 699 Prince Street
     CITY: Alexandria
     STATE: VA
     COUNTRY: USA
     ZIP: 22314
   COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
     SOFTWARE: PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/08/487,550
     FILING DATE: 07-JUN-1995
     CLASSIFICATION: 435
   ATTORNEY/AGENT INFORMATION:
     NAME: Teskin, Robin L.
     REGISTRATION NUMBER: 35,030
     REFERENCE/DOCKET NUMBER: 012712-131
   TELECOMMUNICATION INFORMATION:
     TELEPHONE: 703-836-6620
     TELEFAX: 703-836-2021
   INFORMATION FOR SEQ ID NO: 9:
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       STRANDEDNESS: not relevant
       TOPOLOGY: linear
     MOLECULE TYPE: peptide
     FEATURE:
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US-08-487-550-9

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Matches 711; Conservative   0; Mismatches   0;

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; Sequence 9, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Right column

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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  APPLICATION NUMBER: US/09/526,098
  FILING DATE:
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/383,916
  FILING DATE:
  APPLICATION NUMBER: US 08/487,550
  FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
  NAME: Teskin, Robin L.
  REGISTRATION NUMBER: 35,030
  REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 703-836-6620
  TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
  LENGTH: 711 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: not relevant
  TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
  NAME/KEY: CDS
  LOCATION: 1..711
FEATURE:
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  LOCATION: 1..711
US-09-526-098-9

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Best Local Similarity 100.0%; Pred. No. 2.6e-186; Indels   0; Gaps   0;
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              GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October 2, 2003, 19:53:01 ; Search time 140.653 Seconds
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Perfect score:  711
Sequence:       1 ATGAGGGTCCCGCGCTCAGCT...........CCCCTACAGAATGTTCATGA 711

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Searched:       1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters:    3416838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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          12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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          15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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          17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	711	100.0	711	10	US-09-948-429B-9	Sequence 9, Appli
2	711	100.0	711	12	US-10-124-807-9	Sequence 9, Appli
3	711	100.0	711	12	US-10-291-532-9	Sequence 9, Appli
4	711	100.0	711	13	US-10-124-905-9	Sequence 9, Appli
5	711	100.0	711	13	US-10-073-138-5	Sequence 5, Appli
6	561.8	79.0	1640	14	US-10-198-846-13206	Sequence 13206, A
7	552.6	77.7	768	10	US-09-747-669-4	Sequence 4, Appli
c 8	552.6	77.7	768	14	US-09-747-669-5	Sequence 5, Appli
c 9	552.6	77.7	768	14	US-10-290-703-4	Sequence 4, Appli
c 10	552.6	77.7	768	14	US-10-290-703-5	Sequence 5, Appli
c 11	552.4	77.7	848	14	US-10-158-646-70	Sequence 70, Appl
12	551	77.5	1590	14	US-10-198-846-12799	Sequence 12799, A
13	550.6	77.4	888	14	US-10-158-646-71	Sequence 71, Appl
14	540.2	76.0	705	10	US-09-948-429B-1	Sequence 1, Appli
15	540.2	76.0	705	12	US-10-124-807-1	Sequence 1, Appli
16	540.2	76.0	705	12	US-10-291-532-1	Sequence 1, Appli
17	540.2	76.0	705	13	US-10-124-905-1	Sequence 1, Appli
18	540.2	76.0	705	13	US-10-073-138-1	Sequence 1, Appli
19	534.8	75.2	2112	13	US-10-001-857-108	Sequence 108, App
20	532.2	74.9	915	10	US-09-954-456-788	Sequence 788, App
21	532.2	74.9	915	10	US-09-880-107-3743	Sequence 3743, Ap
22	532.2	74.9	915	12	US-09-873-319-710	Sequence 710, App
23	532.2	74.9	915	12	US-09-960-706-1069	Sequence 1069, Ap
24	531.8	74.8	2635	14	US-10-198-846-13529	Sequence 13529, A
25	527.6	74.2	705	12	US-10-194-801C-3	Sequence 3, Appli
c 26	525.4	73.9	2635	14	US-10-198-846-13529	Sequence 13529, A
c 27	510.6	71.3	1640	14	US-10-198-846-13206	Sequence 13206, A
c 28	507	71.1	1597	14	US-10-198-846-13540	Sequence 13540, A
29	504.2	70.9	883	14	US-10-158-646-73	Sequence 73, Appl
30	494.6	69.6	1597	14	US-10-198-846-13540	Sequence 13540, A
31	484.2	68.1	885	9	US-09-853-161-47	Sequence 47, Appl
32	484.2	68.1	885	9	US-09-852-659A-47	Sequence 47, Appl
33	484.2	68.1	885	9	US-09-852-797-47	Sequence 47, Appl
34	482.6	67.9	879	9	US-09-853-161-29	Sequence 29, Appl
35	482.6	67.9	879	9	US-09-852-659A-29	Sequence 29, Appl
36	482.6	67.9	879	10	US-09-852-797-29	Sequence 29, Appl
c 37	474	66.7	2667	14	US-10-158-646-76	Sequence 76, Appl
38	473	66.5	642	11	US-09-972-655-95	Sequence 95, Appl
39	471.6	66.3	1565	14	US-10-198-846-13276	Sequence 13276, A
40	471.2	66.3	726	12	US-10-225-108A-13	Sequence 13, Appl
c 41	470.4	66.2	895	14	US-10-198-846-12838	Sequence 12838, A
42	468.4	65.9	702	14	US-10-211-357-5	Sequence 5, Appli
43	466.8	65.7	654	11	US-09-972-656-101	Sequence 101, App
44	466.2	65.6	651	11	US-09-972-656-87	Sequence 87, Appl
45	463.4	65.2	648	11	US-09-972-656-89	Sequence 89, Appl

ALIGNMENTS

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RESULT 1
US-09-948-429B-9
; Sequence 9, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/948,429B
;   FILING DATE:
;   CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
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; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/124,807
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   .REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 711 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..711
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: 1..711
US-10-124-807-9

Query Match   100.0%; Score 711; DB 12; Length 711;
Best Local Similarity 100.0%; Pred. No. 5.4e-206;
Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360
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Db 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360

Qy 361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
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Qy 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACCAACAGGCCACTGTGTGTCTCATA 480
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Qy 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
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Qy 541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAAGGCGGCCAGCAGC 600
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Qy 601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGGTCACG 660
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Db 601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGGTCACG 660

Qy 661 CATGAAGGAGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711
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RESULT 2
US-10-124-807-9
; Sequence 9, Application US/10124807
; Publication No. US20030165207A1
; GENERAL INFORMATION:

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                GenCore version 5.1.6
        Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  2, 2003, 08:56:23 ; Search time 27.6933 Seconds
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Title:           US-09-758-173-10
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Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:      1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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    24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB Length	ID	Description
1	1232	100.0	236	19	AAW63764	Macaque primatized
2	1232	100.0	236	23	AAU11645	Protein sequence o
3	1229	99.8	236	18	AAW01821	Primatised anti-hu
4	1052.5	85.4	236	24	AAB36209	Human immune syste
5	1006	81.7	235	20	AAW88465	Monoclonal antibod
6	1001	81.2	236	22	ABG23083	Novel human diagno
7	999.5	81.1	221	23	ABP52959	Human lung specifi
8	992.5	80.6	214	24	ABR01470	Human anti-TIMP-1
9	989	80.3	213	24	ABR01468	Human anti-TIMP-1
10	989	80.3	213	24	ABR01475	Human anti-TIMP-1
11	987	80.1	268	23	ABP62895	Human polypeptide
12	981.5	79.7	214	24	ABR01467	Human anti-TIMP-1
13	979.5	79.5	217	14	AAR42163	Anti-HIV-1 recombi
14	979	79.5	234	24	ABG73422	Human IgG anti-rhe
15	973	79.0	234	18	AAW01817	Primatised anti-hu
16	973	79.0	234	19	AAW63760	Macaque primatized
17	973	79.0	234	23	AAU11538	Protein sequence o
18	971.5	78.9	217	19	AAW40533	Antibody HB4C5 lig
19	969	78.7	242	24	ABU08021	Monoclonal rabies
20	968.5	78.6	248	22	ABG26352	Novel human diagno
21	965	78.3	235	22	AAB36212	Human immune syste
22	965	78.3	235	22	AAB36214	Human immune syste
23	961.5	78.0	219	23	ABG80711	Amyloid peptide co
24	958.5	77.8	216	24	ABR01477	Human anti-TIMP-1
25	958.5	77.8	235	22	ABG19293	Novel human diagno
26	957	77.7	236	22	AAG64472	Human type antihum
27	957	77.7	614	23	ABB06275	Plasmid scFv(CC046
28	955	77.5	235	14	AAR31024	Antibody D light c
29	954	77.4	215	24	ABR01476	Human anti-TIMP-1
30	952.5	77.3	214	24	ABR01487	Human anti-TIMP-1
31	951.5	77.2	216	24	ABR01473	Human anti-TIMP-1
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33	950.5	77.2	214	24	ABR01490	Human anti-TIMP-1
34	950.5	77.2	216	24	ABR01488	Human anti-TIMP-1
35	950.5	77.2	219	21	AAB30594	Variable and first
36	948.5	77.0	214	24	ABR01485	Human anti-TIMP-1
37	947.5	76.9	216	24	ABR01483	Human anti-TIMP-1
38	947	76.9	215	24	ABR01491	Human anti-TIMP-1
39	947	76.9	215	24	ABR01493	Human anti-TIMP-1
40	946	76.8	216	24	ABR01498	Human anti-TIMP-1
41	945.5	76.7	216	24	ABR01482	Human anti-TIMP-1
42	945	76.7	215	24	ABR01464	Human anti-TIMP-1
43	945	76.7	235	22	AAG64474	Human type antihum
44	945	76.7	235	22	AAG64476	Human type antihum
45	944	76.6	215	24	ABR01479	Human anti-TIMP-1

ALIGNMENTS

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RESULT 1
AAW63764
ID   AAW63764 standard; Protein; 236 AA.
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AC   AAW63764;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 16C10 light chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;  97WO-US19906.
XX
PR   08-NOV-1996;  96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35488.
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Left column:

```
XX
PT  New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT  inhibiting binding to CD28 - useful as specific immunosuppressants
PT  for treating diseases that involve interactions between T and B
PT  cells, e.g. graft rejection or tumours
XX
PS  Example 7; Fig 5a; 87pp; English.
XX
CC  This sequence represents a primatized form of the antibody 16C10 light
CC  chain from macaque. This sequence is used in a method which studies new
CC  monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC  B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC  Mab's are specific immunosuppressants for treatment of diseases involving
CC  T cell/B cell interactions, particularly autoimmune disease, specifically
CC  idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC  I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC  inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC  host diseases, B cell lymphoma, infections (including by human immune
CC  deficiency virus) or inflammatory disease and tumours. Optionally the
CC  MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC  also be used as imaging agents and as vaccines or immunogens to develop
CC  anti-idiotype reagents. MAb's are optionally combined with other proteins
CC  or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC  induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC  production of interleukin-2 (IL-2), T cell proliferation and
CC  antigen-specific immunoglobulin G (IgG) responses.
XX
SQ  Sequence 236 AA;

Query Match          100.0%;  Score 1232;  DB 19;  Length 236;
Best Local Similarity 100.0%;  Pred. No. 1.2e-66;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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Qy 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
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Qy 181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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Db 181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 2
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ID  AAU11645 standard; Protein; 236 AA.
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AC  AAU11645;
XX
DT  12-MAR-2002 (first entry)
XX
DE  Protein sequence of primatised form of the light chain of 16C10 antibody.
XX
KW  Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW  neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW  B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW  tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW  graft-vs-host disease; immunosuppression; organ rejection;
KW  interleukin-2; IL-2; mutant; mutein.
XX
OS  Chimeric - Homo sapiens.
OS  Chimeric - Macaca sp.
OS  Synthetic.
XX
PN  WO200189567-A1.
XX
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Right column:

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PD  29-NOV-2001.
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PF  22-MAY-2001; 2001WO-US16364.
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PR  22-MAY-2000; 2000US-0576424.
XX
PA  (IDEC-) IDEC PHARM CORP.
XX
PI  Anderson DR, Hanna N, Brams P;
XX
DR  WPI; 2002-089895/12.
DR  N-PSDB; AAS17246.
XX
PT  Use of monoclonal antibody which specifically binds to B7.1 antigen
PT  CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT  treating cancer, graft-vs-host disease and autoimmune disease such as
PT  allergy -
XX
PS  Example 8; Fig 5a; 89pp; English.
XX
CC  The present invention relates to a new use of a monoclonal antibody
CC  which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC  (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC  useful for treating diseases such as B cell cancer, lymphoma, a
CC  cancer where B cells promote the growth and/or metastasis of tumours,
CC  B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC  idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC  type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC  anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC  or graft-vs-host disease. The antibody is useful for immunosuppression
CC  in a human or animal and for treating or preventing resistance to or
CC  rejection of transplanted organ or tissue for treating proliferative
CC  and hyperproliferative diseases, for treating reversible obstructive
CC  airways disease, intestinal inflammations and allergies e.g. Crohn's
CC  disease and ulcerative colitis, food-related allergies e.g. migraine,
CC  rhinitis and eczema, and other types of allergies. The present protein
CC  sequence represents the light chain of 16C10, a primatised antibody
CC  used in the invention to induce apoptosis and inhibit production of
CC  interleukin-2 (IL-2).
XX
SQ  Sequence 236 AA;

Query Match          100.0%;  Score 1232;  DB 23;  Length 236;
Best Local Similarity 100.0%;  Pred. No. 1.2e-66;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60

Qy  61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy 181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 3
AAW01821
ID  AAW01821 standard; Protein; 236 AA.
XX
AC  AAW01821;
XX
DT  25-MAY-1997 (first entry)
XX
DE  Primatised anti-human B7.1 antigen antibody 16C10 light chain.
XX
```

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     October  2, 2003, 09:07:34  ; Search time 10.3712 seconds
                                           (without alignments)
                                           2188.349 Million cell updates/sec

Title:      US-09-758-173-10
Perfect score: 1232
Sequence:   1 MRVPAQLLGLLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:   283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:     283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR.76:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1027	83.4	235	2	S05270	Ig lambda chain pr
2	1014	82.3	233	2	S25752	Ig lambda chain -
3	1010.5	82.0	236	2	S25746	Ig lambda chain -
4	1006	81.7	216	2	S29258	Ig lambda chain -
5	1006	81.7	234	2	S25757	Ig lambda chain v
6	1003.5	81.5	217	2	JE0246	Ig lambda chain NI
7	1001	81.2	235	2	S25750	Ig lambda chain -
8	995	80.8	232	2	S25742	Ig lambda chain -
9	989.5	80.3	213	2	S21066	Ig lambda chain V
10	987	80.1	233	2	S25744	Ig lambda chain -
11	986	80.0	216	2	A42193	Ig lambda chain (B
12	967.5	78.5	235	2	S25754	Ig lambda chain -
13	946	76.8	216	2	S03401	Ig lambda chain (K
14	944	76.6	235	2	S14675	Ig lambda chain -
15	942	76.5	208	2	B49444	Ig lambda chain (N
16	934	75.8	235	2	S25759	Ig lambda chain -
17	923	74.9	235	2	S25758	Ig lambda chain -
18	894	72.6	232	2	S25756	Ig lambda chain NI
19	884	71.8	216	2	JE0245	Ig lambda chain -
20	879	71.3	233	2	S25748	Ig lambda chain -
21	877	71.2	231	2	S25738	Ig lambda chain -
22	875	71.0	233	2	S25741	Ig lambda chain NI
23	872.5	70.8	233	2	S25747	Ig lambda chain -
24	866	70.3	231	2	S25751	Ig lambda chain -
25	861	69.9	216	2	S69130	Ig lambda chain (D
26	850	69.0	231	2	S25753	Ig lambda chain -
27	846.5	68.7	235	2	S25749	Ig lambda chain NI
28	839	68.1	213	2	JE0247	Ig lambda chain NI
29	839	68.1	226	2	S25745	Ig lambda chain -
30	815	66.2	190	2	S25740	Ig lambda chain -
31	811	65.8	243	2	S25755	Ig lambda chain -
32	737.5	59.9	212	2	S70431	Ig lambda chain V-
33	649.5	52.7	181	2	PT0220	Ig lambda chain pr
34	644.5	52.3	232	2	S17399	Ig lambda chain -
35	643	52.2	230	2	S49949	Ig light chain pre
36	630.5	51.2	213	2	A21177	Ig lambda chain v
37	625.5	50.8	214	2	PC4156	Ig lambda chain (K
38	606	49.2	118	2	S12441	Ig lambda chain (K
39	603	48.9	118	2	S12442	Ig lambda chain (K
40	581	47.2	118	2	S12443	Ig lambda chain (M
41	576	46.8	118	2	S12440	Ig lambda chain J-
42	573	46.5	118	2	A39949	Ig lambda chain -
43	550	44.6	234	2	A39956	Ig lambda chain pr
44	548	44.5	105	1	L2HU	Ig lambda chain C
45	547.5	44.4	149	2	S23626	Ig lambda chain V

ALIGNMENTS

```
RESULT 1
S05270
Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S05270; S04601
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05270
A;Molecule type: mRNA
A;Residues: 1-235 <KIS1>
A;Cross-references: EMBL:X14583; NID:g33394; PIDN:g33394; PID:CAA32725.1; PID:g33395
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains
A;Reference number: S04601; MUID:89296497; PMID:2500644
A;Accession: S04601
A;Molecule type: mRNA
A;Residues: 1-130 <KIS2>
A;Cross-references: EMBL:X14583
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-235/Product: Ig lambda chain #status predicted <MAT>
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match              83.4%;  Score 1027;  DB 2;  Length 235;
Best Local Similarity    87.0%;  Pred. No. 7.8e-60;
Matches  200;  Conservative  12;  Mismatches  18;  Indels  0;  Gaps  0;

Qy       7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
             ||||:||||||||||| ||||||:||||||||||||:|||||||||||||||||||||
Db       6 LLLTLLIHCTGSWAQSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNVSWYQQLPGTAPK 65

Qy      67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYCQSYDSSLNAQVFGGGTR 126
            |||||:||||||||| |||||||||||:|||:| |||||||||||| :|||:||||||||
Db      66 LLIYDNNKRPSGIPDRFSGSKSGTSATLGITLGITGLQTGDEADYCGTWDSSLSAGVFGGGTK 125

Qy     127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

Qy     187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVAPTECS 235

RESULT 2
S25752
Ig lambda chain - human
C;Species: Homo sapiens (man)
```

RESULT 3
S25746
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25746
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-236 <COM>
A;Cross-references: EMBL:X57811; NID:g33721; PIDN:CAA40948.1; PID:g33722
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;151-219/Domain: immunoglobulin homology <IMM>

Query Match   82.0%; Score 1010.5; DB 2; Length 235;
Best Local Similarity   84.4%; Pred. No. 9.1e-59;
Matches 195; Conservative 16; Mismatches 19; Indels   1; Gaps   1;

Qy   7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
          |||| |||| |: |||||||||||||| || | | || |: ||::|||||||||||
Db   6 LLLTLLAHCTGSWAQSVLTQPPSASGTPGQRVTISCSGSTSNIGAGHVHWYQQVPGTAP 65

Qy   66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSLNAQVFGGGT 125
         ||||| : :||| ||||||||||||||| || :| | :|||| |||||||| | |
Db   66 KLLIYADNNRPSGVPDRISGSKSGTAASLAITGLRAEDEADYYCQSFDSSLSGWVFGGAT 125

Qy 126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
         | ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db 126 KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185

Qy 186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 4
S29258
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jan-2000
C;Accession: S29258
R;Chouchane, L.; van Sprosnen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
Eur. J. Biochem. 207, 1115-1121, 1992
A;Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segmen
A;Reference number: S29257; MUID:92362614; PMID:1499555
A;Accession: S29258
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-216 <CHO>
A;Note: only part of the coding sequence is given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: pyroglutamic acid
F;1/Domain: immunoglobulin homology <IMM>
F;131-199/Domain: immunoglobulin V region; immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

Query Match   81.7%; Score 1006; DB 2; Length 216;
Best Local Similarity   89.9%; Pred. No. 1.6e-58;
Matches 195; Conservative   9; Mismatches 11; Indels   2; Gaps   2;

Qy   21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGG-YDLHWYQQLPGTAPKLLIYDINKRPSGI 79
          :||||||||||||||||||||||||||||:: :|::||||||||||||||||||||||:
Db   1 QSVLTQPPSVSGAPGQRVTISCTGSSNIGARYDVNWYQQLPGTAPKLLIYGNTIRPSGV 60

Qy   80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAAPSV 139
         :||||||||||||||||||| |||:|||||||| |::||| |||||: |||||||||||
Db   61 PDRFSGSKSGTSASLAITGLQAEDEGDYYCQTYDISLTV-VFGGGTKLTVLGQPKAAPSV 119

Qy 140 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 120 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 179

Qy 200 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||
Db 180 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 216

RESULT 5
S25757
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25757
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25757
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-234 <COM>
A;Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;149-217/Domain: immunoglobulin homology <IMM>

Query Match   81.7%; Score 1006; DB 2; Length 234;
Best Local Similarity   83.0%; Pred. No. 1.8e-58;
Matches 191; Conservative 20; Mismatches 19; Indels   0; Gaps   0;

Qy   7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
          || ||| || :|||||||||||||||||||||:|||: :||::|||||||||||||
Db   5 LLLTLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGSTSNIGSNTVNWYQQLPGTAPK 64

Qy   67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
         |||| : ::||| :: |||| || | |||| |: :||:|||| : ||| ||| |||:

```
                    GenCore version 5.1.6
              Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:       October  2, 2003, 08:56:23  ; Search time 6.50958 Seconds
                                             (without alignments)
                                             1704.917 Million cell updates/sec

Title:        US-09-758-173-10
Perfect score: 1232
Sequence:     1 MRVPAQLLGLLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 236

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:      127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_41:*

                                    SUMMARIES

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.
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Result No.	Score	% Match	Query Length	DB	ID	Description		
1	548	44.5	105	1	LAC_HUMAN	P01842	homo	sapien
2	527	42.8	213	1	ILL1_HUMAN	P15814	homo	sapien
3	463	37.6	130	1	LV1G_HUMAN	P06316	homo	sapien
4	454	36.9	111	1	LV1D_HUMAN	P01702	homo	sapien
5	432	35.1	111	1	LV1C_HUMAN	P01701	homo	sapien
6	426	34.6	109	1	LV1F_HUMAN	P04208	homo	sapien
7	424.5	34.5	112	1	LV2K_HUMAN	P04209	homo	sapien
8	415	33.7	105	1	LAC_PIG	P01846	sus	scrofa
9	413.5	33.6	112	1	LV1H_HUMAN	P06887	homo	sapien
10	412	33.4	105	1	LAC1_MOUSE	P01843	mus	musculu
11	407.5	33.1	112	1	LV1B_HUMAN	P01704	homo	sapien
12	402	32.6	109	1	LV1I_HUMAN	P06888	homo	sapien
13	399	32.4	105	1	LAC_RABIT	P01847	oryctolagus	
14	396	32.1	111	1	LV1A_HUMAN	P01699	homo	sapien
15	396	32.1	111	1	LV2B_HUMAN	P01705	homo	sapien
16	395	32.1	111	1	LV2H_HUMAN	P01711	homo	sapien
17	393	31.9	103	1	LV1E_HUMAN	P01703	homo	sapien
18	392	31.8	111	1	LV2F_HUMAN	P01709	homo	sapien
19	391	31.7	111	1	LV2I_HUMAN	P01712	homo	sapien
20	385.5	31.3	104	1	LAC1_RAT	P20766	rattus	norv
21	381	30.9	111	1	LV2D_HUMAN	P01707	homo	sapien
22	380.5	30.9	104	1	LAC2_RAT	P20767	rattus	norv
23	377	30.6	105	1	LAC5_MUSSP	P20765	mus	spretus
24	374.5	30.4	104	1	LAC3_MOUSE	P01845	mus	musculu
25	372	30.2	111	1	LV2A_HUMAN	P01704	homo	sapien
26	371	30.1	111	1	LV2C_HUMAN	P01706	homo	sapien
27	370	30.0	109	1	LV2E_HUMAN	P01708	homo	sapien
28	369.5	30.0	104	1	LAC2_MOUSE	P01844	mus	musculu
29	368	29.9	111	1	LV2G_HUMAN	P01710	homo	sapien
30	352.5	28.6	110	1	LV2J_HUMAN	P01713	homo	sapien
31	347	28.2	105	1	LAC5_MOUSE	P20764	mus	musculu
32	344.5	28.0	112	1	LV6A_HUMAN	P01721	homo	sapien
33	342	27.8	111	1	LV6C_HUMAN	P06317	homo	sapien
34	341	27.7	111	1	LV6D_HUMAN	P06318	homo	sapien
35	340.5	27.6	129	1	KV1W_HUMAN	P04431	homo	sapien
36	339	27.5	108	1	LV3A_HUMAN	P01714	homo	sapien
37	339	27.5	111	1	LV3B_HUMAN	P80748	homo	sapien
38	334.5	27.2	131	1	LV6E_HUMAN	P06319	homo	sapien
39	329.5	26.7	117	1	KV1J_HUMAN	P01602	homo	sapien
40	326.5	26.5	103	1	LAC_CHICK	P20763	gallus	gall
41	326	26.5	106	1	LV4E_HUMAN	P06889	homo	sapien
42	322	26.1	108	1	LV5A_HUMAN	P01719	homo	sapien
43	319	25.9	106	1	LV4B_HUMAN	P01716	homo	sapien
44	318	25.8	106	1	LV4A_HUMAN	P01715	homo	sapien
45	314	25.5	111	1	LV2L_HUMAN	P80422	homo	sapien

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                                    ALIGNMENTS

RESULT 1
LAC_HUMAN
ID   LAC_HUMAN      STANDARD;       PRT;    105 AA.
AC   P01842; P80423;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain C regions.
GN   IGLC1 AND IGLC2 AND IGLC3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (BENCE-JONES PROTEIN SH).
RX   MEDLINE=70166723; PubMed=4909564;
RA   Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT   complete amino acid sequence and the location of the disulfide
RT   bridges.";
RL   J. Biol. Chem. 245:2171-2176(1970).
RN   [2]
RP   SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RX   MEDLINE=69088380; PubMed=4883841;
RA   Milstein C., Clegg J.B., Jarvis J.M.;
RT   "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT   Bence-Jones protein.";
RL   Biochem. J. 110:631-652(1968).
RN   [3]
RP   SEQUENCE (BENCE-JONES PROTEIN NIG-64).
RX   MEDLINE=83186114; PubMed=6404900;
RA   Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA   Shimizu A.;
RT   "Comparative studies on the structure of the light chains of human
RT   immunoglobulins. IV. Assignment of a subsubgroup.";
RL   J. Biochem. 93:421-429(1983).
RN   [4]
RP   SEQUENCE (BENCE-JONES PROTEIN KERN).
RX   MEDLINE=71150336; PubMed=5549568;
RA   Ponstingl H., Hess M., Hilschmann N.;
RT   "Structural rule of antibodies. Primary structure of a monoclonal
RT   immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
RT   protein Kern). V. The complete amino acid sequence and its genetic
RT   interpretation."; v.
RL   Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
RN   [5]
RP   PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
RX   MEDLINE=74109253; PubMed=4814727;
RA   Chen B.L., Poljak R.J.;
RT   "Amino acid sequence of the (lambda) light chain of a human myeloma
RT   immunoglobulin (IgG New).";
RL   Biochemistry 13:1295-1302(1974).
RN   [6]
RP   SEQUENCE (DCT).
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
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RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
RX   MEDLINE=75046825; PubMed=4215080;
RA   Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
RA   Saul F.;
RT   "The three-dimensional structure of the fab' fragment of a human
RT   myeloma immunoglobulin at 2.0-A resolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
RN   [8]
RP   PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
RX   MEDLINE=75013804; PubMed=4415202;
RA   Fett J.W., Deutsch H.F.;
RT   "Primary structure of the Mcg lambda chain.";
RL   Biochemistry 13:4102-4114(1974).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
RA   Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA   Panagiotopoulos N.;
RT   "Rotational allomerism and divergent evolution of domains in
RT   immunoglobulin light chains.";
RL   Biochemistry 14:3953-3961(1975).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY OF MCG.
RX   MEDLINE=90133913; PubMed=2515285;
RA   Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT   "Three-dimensional structure of a light chain dimer crystallized in
RT   water. Conformational flexibility of a molecule in two crystal
RT   forms.";
RL   J. Mol. Biol. 210:601-615(1989).
RN   [11]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82080680; PubMed=6273747;
RA   Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
RT   "Clustered arrangement of immunoglobulin lambda constant region genes
RT   in man.";
RL   Nature 294:536-540(1981).
CC   -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN
CC       FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE
CC       KERN+ MARKER, THE NEWM PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN
CC       HAS THE KERN+ MARKER, AND THE MCG+ MARKER.
CC   -!- MISCELLANEOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE
CC       3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE
CC       (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
CC       SEQUENCE (LAMBDA-3).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00253; AAA59107.1; -.
DR   EMBL; L38562; AAB36581.1; ALT_INIT.
DR   EMBL; X51754; CAB38569.1; ALT_INIT.
DR   EMBL; X51755; CAA36049.1; -.
DR   EMBL; X51755; CAA36051.1; -.
DR   PIR; A92057; L2HU.
DR   PDB; 2MCG; 15-JUL-92.
DR   PDB; 7FAB; 31-JAN-94.
DR   PDB; 1AOK; 04-FEB-98.
DR   PDB; 1I1L; 15-MAY-97.
DR   Genew; HGNC:5855; IGLC1.
DR   Genew; HGNC:5856; IGLC2.
DR   Genew; HGNC:5857; IGLC3.
DR   MIM; 147220; -.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
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DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Bence-Jones protein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        6    100       IG-LIKE.
FT   DISULFID     27     86
FT   DISULFID    104    104       INTERCHAIN (WITH HEAVY CHAIN).
FT   VARIANT       5      5       A -> N (IN MCG+ MARKER).
FT                                /FTId=VAR_003898.
FT   VARIANT       7      7       S -> T (IN MCG+ MARKER).
FT                                /FTId=VAR_003899.
FT   VARIANT      45     45       S -> G (IN KERN+ MARKER).
FT                                /FTId=VAR_003900.
FT   VARIANT      56     56       T -> K (IN MCG+ MARKER).
FT                                /FTId=VAR_003901.
FT   VARIANT      82     82       R -> K (IN OZ+ MARKER).
FT                                /FTId=VAR_003902.
FT   STRAND        8     11
FT   HELIX        15     19
FT   TURN         20     21
FT   STRAND       24     32
FT   STRAND       38     43
FT   TURN         44     45
FT   STRAND       46     48
FT   STRAND       52     59
FT   TURN         61     62
FT   STRAND       65     72
FT   HELIX        75     80
FT   STRAND       84     89
FT   STRAND       94     99
SQ   SEQUENCE   105 AA;  11236 MW;  DCD9C7C201C13CC2 CRC64;

Query Match             44.5%;  Score 548;  DB 1;  Length 105;
Best Local Similarity   100.0%;  Pred. No. 1.2e-36;
Matches   105;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 60

Qy        192 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
              |||||||||||||||||||||||||||||||||||||||||||||
Db         61 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 105

RESULT 2
ILL1_HUMAN
ID   ILL1_HUMAN     STANDARD;      PRT;     213 AA.
AC   P15814;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-
DE   related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
DE   (CD179b antigen).
GN   IGLL1 OR IGLL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89315835; PubMed=2501791;
RA   Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
RA   McKearn J.P.;
RT   "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
RT   expressed in pre-B cells and may encode the human immunoglobulin
```

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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      October  2, 2003, 08:56:23  ; Search time 22.8387 Seconds
                                     (without alignments)
                                     2666.544 Million cell updates/sec

Title:       US-09-758-173-10
Perfect score: 1232
Sequence:    1 MRVPAQLLGLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 236

Scoring table:: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    830525 seqs, 25805204 residues

Total number of hits,satisfying chosen parameters:    830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_23:*
         1: sp_archea:*
         2: sp_bacteria:*
         3: sp_fungi:*
         4: sp_human:*
         5: sp_invertebrate:*
         6: sp_mammal:*
         7: sp_mhc:*
         8: sp_organelle:*
         9: sp_phage:*
        10: sp_plant:*
        11: sp_rodent:*
        12: sp_virus:*
        13: sp_vertebrate:*
        14: sp_unclassified:*
        15: sp_rvirus:*
        16: sp_bacteriap:*
        17: sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description			
1	1045	84.8	237	4	Q8WUK4	Q8wuk4 homo sapien	Q91W12	17	466 37.8	Q91W12 mus musculu
2	1045	84.8	237	4	Q8WTU6	Q8wtu6 homo sapien	Q8R062	18	464.5 37.7	Q8R062 mus musculu
3	991.5	80.5	236	4	Q96E61	Q96e61 homo sapien	Q8VCI6	19	461.5 37.5	Q8vci6 mus musculu
4	977.5	79.3	236	4	Q8NEJ1	Q8nej1 homo sapien	Q99M37	20	453.5 36.8	Q99m37 mus musculu
5	891	72.3	234	4	Q8N355	Q8n355 homo sapien	Q91WS9	21	450.5 36.6	Q91ws9 mus musculu
6	888	72.1	233	4	Q8TBC9	Q8tbc9 homo sapien	Q91WF8	22	447.5 36.3	Q91wf8 mus musculu
7	871	70.7	233	4	Q8N5F4	Q8n5f4 homo sapien	Q8TE63	23	439 35.6	Q8te63 homo sapien
8	805.5	65.4	233	4	Q96I69	Q96i69 homo sapien	Q8VC55	24	439 35.6	Q8vc55 mus musculu
9	767.5	62.3	240	4	Q8WUK3	Q8wuk3 homo sapien	Q8R028	25	433.5 35.2	Q8r028 mus musculu
10	722	58.6	235	11	Q99M11	Q99m11 mus musculu	Q8K0F8	26	415 33.7	Q8k0f8 mus musculu
11	551	44.7	234	4	Q8TCJ5	Q8tcj5 homo sapien	Q9R1A5	27	410.5 33.3	Q9r1a5 mus musculu
12	496.5	40.3	106	4	Q8NEK1	Q8nek1 homo sapien	Q8IZD8	28	396 32.1	Q8izd8 homo sapien
13	488.5	39.7	234	11	Q8VCP0	Q8vcp0 mus musculu	Q96SB0	29	385 31.2	Q96sb0 homo sapien
14	472	38.3	130	11	Q9D8W4	Q9d8w4 mus musculu	Q96JD0	30	378 30.7	Q96jd0 homo sapien
15	472	38.3	239	4	Q8TCD0	Q8tcd0 homo sapien	Q99JC1	31	375.5 30.5	Q99jc1 mus musculu
16	469	38.1	239	4	Q8NEK0	Q8nek0 homo sapien	Q96JD2	32	373 30.3	Q96jd2 homo sapien
							Q96JD1	33	349.5 28.4	Q96jd1 homo sapien
							Q9NSD6	34	332 26.9	Q9nsd6 homo sapien
							Q90544	35	292.5 23.7	Q90544 ginglymosto
							Q9UL82	36	287.5 23.3	Q9ul82 homo sapien
							Q90524	37	283 23.0	Q90524 ginglymosto
							Q925S9	38	282.5 22.9	Q925s9 mus musculu
							Q8K1F1	39	266.5 21.8	Q8k1f1 mus musculu
							Q90529	40	268.5 21.8	Q90529 ginglymosto
							Q8K1F0	41	267.5 21.7	Q8k1f0 mus musculu
							Q8VDD0	42	265.5 21.6	Q8vdd0 mus musculu
							Q9UL78	43	262 21.3	Q9ul78 homo sapien
							Q8TC77	44	260 21.1	Q8tc77 homo sapien
							Q90536	45	258 20.9	Q90536 ginglymosto

ALIGNMENTS

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RESULT 1
Q8WUK4
ID   Q8WUK4       PRELIMINARY;       PRI;       237 AA.
AC   Q8WUK4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020233; AAH20233.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE  237 AA;  24897 MW;  73C7D70B8039D186 CRC64;
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Query Match             84.8%;      Score 1045;      DB 4;      Length 237;
Best Local Similarity   88.4%;      Pred. No. 2.2e-83;
Matches  205;  Conservative  10;  Mismatches  15;  Indels  2;  Gaps  2;

Qy      7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
          ||  ||  |: ||::||||||||| |||||| ||||||||||:|| :||||||||||||
Db      6 LLTLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP 65

Qy     66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNA-QVFGGG 124
          |||| : |||:|||:||||||||||||||:|||||| || |||||| ||  ||||  |||
Db     66 KLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGFVVFGGG 125

Qy    125 TRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 184
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Db   126  TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE  185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   185  TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  237

RESULT 2
Q8WTU6
ID   Q8WTU6;             PRELIMINARY;      PRT;     237 AA.
AC   Q8WTU6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022098; AAH22098.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE  237 AA;  24884 MW;  E6CF371E75396BE8 CRC64;

Query Match             84.8%;  Score 1045;  DB 4;  Length 237;
Best Local Similarity   88.4%;  Pred. No. 2.2e-83;
Matches  205;  Conservative  10;  Mismatches  15;  Indels  2;  Gaps  2;

Qy     7  LLGLLLWLPLGARCESVLTQPPSVSGAPGQKVTISCTGSTNIG-GYDLHWYQQLPGTAP  65
          ||| ||   |: .||||||||||||||||||: ||||||| ||| |||:||||||||||
Db     6  LLLTLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP  65
Qy    66  KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGG  124
          ||||| || ||||| ||||||||||:|||||||||| :||||||||||||| ||: |||||
Db    66  KLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDYSLSASGVFGGG  125
Qy   125  TRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE  184
          |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126  TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE  185
Qy   185  TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  237

RESULT 3
Q96E61
ID   Q96E61;             PRELIMINARY;      PRT;     236 AA.
AC   Q96E61;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
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RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012876; AAH12876.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE  236 AA;  24712 MW;  7EC9FB3622FED957 CRC64;

Query Match             80.5%;  Score 991.5;  DB 4;  Length 236;
Best Local Similarity   83.1%;  Pred. No. 1e-78;
Matches  192;  Conservative  12;  Mismatches  26;  Indels  1;  Gaps  1;

Qy     7  LLGLLLWLPLGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP  65
          ||| ||   |: .|||||||:|||||||||||:||||||| ||| |||:|||||| |||
Db     6  LLLTLLAHCTGSWAQSVLAQPPSVSGAPGQTVTISCTGSSTNIGAGYAVHWYQQFPGAAP  65
Qy    66  KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT  125
          |:|||| |||||||| ||||||||||:|||||||||| :||||||||||||| |:|:.||
Db    66  KVLIYGNYNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGAGT  125
Qy   126  RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET  185
          :||||||||| |:|||||||||||||||||:|||||||||||||||||||||:||||||
Db   126  KVTVLGQPKANPTVLFPPSSEELQANKAILVCLISDFYPGAVTVAWKADGSPVKAGVET  185
Qy   186  TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
          | ||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  TKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236

RESULT 4
Q8NEJ1
ID   Q8NEJ1;             PRELIMINARY;      PRT;     236 AA.
AC   Q8NEJ1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC030984; AAH30984.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE  236 AA;  25024 MW;  1703B7794263OE08 CRC64;

Query Match             79.3%;  Score 977.5;  DB 4;  Pred. No. 1.7e-77;
Best Local Similarity   81.8%;  Pred. No. 1.7e-77;
Matches  189;  Conservative  20;  Mismatches  21;  Indels  1;  Gaps  1;

Qy     7  LLGLLLWLPLGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK  66
          ||| ||   .|: .||||||||||:||.|||:|||||.||:|||||::: ||| |||||
Db     6  LLLTLLTHCAGSWAQSVLTQPPSASGSPGQRVTISCSGSRSNIGSNYVYWQQVPGTAPK  65
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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      October  2, 2003, 09:12:09  ; Search time 10.4815 Seconds
                                           (without alignments)
                                           952.662 Million cell updates/sec

Title:       US-09-758-173-10
Perfect score: 1232
Sequence:    1 MRVPAQLLGLLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    328717 segs, 42310858 residues

Total number of hits satisfying chosen parameters:   328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1232	100.0	236	3	US-09-526-098-10	Sequence 10, Appl
3	1052.5	85.4	236	3	US-09-049-672A-7	Sequence 7, Appl
4	979	79.5	234	3	US-09-372-425A-4	Sequence 4, Appl
5	973	79.0	234	3	US-08-487-550-2	Sequence 2, Appl
6	973	79.0	234	4	US-09-526-098-2	Sequence 2, Appl
7	965	78.3	235	3	US-09-049-672A-10	Sequence 10, Appl
8	965	78.3	235	3	US-09-049-672A-12	Sequence 12, Appl
9	955	77.5	235	4	US-08-378-939-12	Sequence 12, Appl
10	955	77.5	235	4	US-09-152-060-70	Sequence 70, Appl
11	885	71.8	235	3	US-09-152-060-88	Sequence 88, Appl
12	882	71.6	233	3	US-08-523-894-6	Sequence 6, Appl
13	857.5	69.6	240	3	US-09-049-672A-11	Sequence 11, Appl
14	836	67.9	238	4	US-08-793-450-6	Sequence 6, Appl
15	804.5	65.3	229	4	US-08-751-359-22	Sequence 22, Appl
16	634.5	51.5	229	4	US-08-907-146-22	Sequence 22, Appl
17	634.5	51.5	109	2	US-08-761-277A-51	Sequence 51, Appl
18	567	46.0	105	1	US-08-422-101-9	Sequence 9, Appl
19	548	44.5	105	2	US-08-422-091-9	Sequence 9, Appl
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21	548	44.5	105	3	US-08-788-800-6	Sequence 6, Appl
22	548	44.5	105	3	US-08-422-093-9	Sequence 9, Appli
23	548	44.5	105	3	US-08-422-112-9	Sequence 9, Appli
24	544.5	44.2	200	6	5189147-10	Patent No. 5189147
25	543	44.1	106	4	US-09-313-942-14	Sequence 14, Appl
26	535	43.4	104	4	US-09-025-769B-170	Sequence 170, App
27	522	42.4	241	2	US-07-916-098A-56	Sequence 56, Appl

28	508.5	41.3	236	1	US-08-157-101A-5	Sequence 5, Appli
29	508	41.2	235	1	US-08-276-852-153	Sequence 153, App
30	508	41.2	235	1	US-08-899-575-153	Sequence 153, App
31	508	41.2	235	1	US-08-899-575-153	Sequence 153, App
32	508	41.2	235	5	PCT-US95-08743-153	Sequence 153, App
33	502.5	40.8	235	5	US-08-812-586-16	Sequence 16, Appl
34	502.5	40.8	235	4	US-09-535-832A-17	Sequence 17, Appl
35	499	40.5	234	4	US-09-740-002-26	Sequence 26, Appl
36	496.5	40.3	131	1	US-08-305-683A-4	Sequence 4, Appl
37	492.5	40.0	234	5	US-09-04-672A-6	Sequence 6, Appli
38	492.5	40.0	234	1	PCT-US94-07659-4	Sequence 4, Appli
39	492.5	40.0	310	4	US-09-079-029-11	Sequence 11, Appl
40	484.5	39.3	234	4	US-09-740-002-24	Sequence 24, Appl
41	483	39.2	242	4	US-09-479-614-20	Sequence 20, Appl
42	482.5	39.2	234	2	US-07-690-19-2	Sequence 2, Appli
43	476	38.6	112	4	US-09-025-769B-18	Sequence 18, Appl
44	475	38.6	239	1	US-08-353-400-37	Sequence 37, Appl
45	472	38.3	239	3	US-08-487-550-6	Sequence 6, Appli

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                              ALIGNMENTS

RESULT 1
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; Sequence 10, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION:   TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION:   PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION:   IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES:  12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;   STREET:  699 Prince Street
;   CITY:  Alexandria
;   STATE:  VA
;   COUNTRY:  USA
;   ZIP:  22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/487,550
;   FILING DATE:  07-JUN-1995
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME:  Teskin, Robin L.
;   REGISTRATION NUMBER:  35,030
;  REFERENCE/DOCKET NUMBER:  012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  703-836-6620
;   TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  10:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 236 amino acids
;    TYPE:  amino acid
;    TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-487-550-10

  Query Match             100.0%;  Score 1232;  DB 3;  Length 236;
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  Matches  236;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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; Sequence 10, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/526,098
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 236 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-526-098-10

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Best Local Similarity  100.0%;  Pred. No. 1.7e-91;
Matches  236;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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RESULT 3
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; Sequence 7, Application US/09049672A
; Patent No.6135941
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Yue, Henry
;   APPLICANT: Au-Young, Janice
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Guegler, Karl J.
;   APPLICANT: Baughn, Mariah R.
;   TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/049,672A
;   FILING DATE: HEREWITH
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Cerrone, Michael C
;   REGISTRATION NUMBER: 39,132
;   REFERENCE/DOCKET NUMBER: PF-0497 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
;   TELEX:
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 236 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: ADRETUT05
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US-09-049-672A-7

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               Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   October  2, 2003, 09:18:44 ; Search time 88.5965 Seconds
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Perfect score: 1232
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Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters:        587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	1232	100.0	236	12	US-10-291-532-10	Sequence 10, Appl
4	1232	100.0	236	14	US-10-124-905-10	Sequence 10, Appl
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7	999.5	81.1	221	14	US-10-001-857-202	Sequence 202, App
8	974	79.1	234	12	US-10-194-801C-4	Sequence 4, Appli
9	973	79.0	234	10	US-09-948-429B-2	Sequence 2, Appli
10	973	79.0	234	12	US-10-124-807-2	Sequence 2, Appli
11	973	79.0	234	12	US-10-291-532-2	Sequence 2, Appli
12	973	79.0	234	14	US-10-124-905-2	Sequence 2, Appli
13	969	78.7	242	12	US-10-225-108A-14	Sequence 14, Appl
14	950.5	77.2	219	10	US-09-097-449-38	Sequence 38, Appl
15	916.5	74.4	219	15	US-10-026-925-57	Sequence 57, Appl
16	910	73.9	214	11	US-09-972-656-96	Sequence 96, Appl
17	909	73.8	218	11	US-09-972-656-102	Sequence 102, App
18	907.5	73.7	217	11	US-09-972-656-88	Sequence 88, Appl
19	897	72.8	216	11	US-09-972-656-90	Sequence 90, Appl
20	888	72.1	218	11	US-09-791-153A-51	Sequence 51, Appl
21	886	71.9	216	11	US-09-972-655-108	Sequence 108, App
22	885	71.8	235	9	US-09-853-161-70	Sequence 70, Appl
23	885	71.8	235	9	US-09-852-659A-70	Sequence 70, Appl
24	885	71.8	235	10	US-09-852-797-70	Sequence 70, Appl
25	882	71.6	235	9	US-09-853-161-88	Sequence 88, Appl
26	882	71.6	235	9	US-09-852-659A-88	Sequence 88, Appl
27	882	71.6	235	10	US-09-852-797-88	Sequence 88, Appl
28	876.5	71.1	235	12	US-10-076-747-82	Sequence 82, Appl
29	868	70.5	232	12	US-10-225-108A-12	Sequence 12, Appl
30	860.5	69.8	229	12	US-10-310-719-36	Sequence 36, Appl
31	857.5	69.6	233	15	US-10-211-357-6	Sequence 6, Appli
32	854.5	69.4	244	9	US-09-925-301-1424	Sequence 1424, Ap
33	841	68.3	212	11	US-09-972-656-98	Sequence 98, Appl
34	826	67.0	239	10	US-09-828-995B-26	Sequence 26, Appl
35	815.5	66.3	239	15	US-10-221-945-2	Sequence 2, Appli
36	815	66.2	216	10	US-09-736-371B-19	Sequence 19, Appl
37	762.5	61.9	246	11	US-09-909-567B-49	Sequence 49, Appl
38	683.5	55.5	216	9	US-09-291-299A-8	Sequence 8, Appli
39	673	54.6	217	9	US-09-291-299A-7	Sequence 7, Appli
40	639.5	51.9	216	9	US-09-291-299A-9	Sequence 9, Appli
41	635.5	51.6	216	9	US-09-291-299A-10	Sequence 10, Appl
42	569.5	46.2	147	11	US-09-988-115A-57	Sequence 57, Appl
43	567	46.0	109	10	US-09-925-664-51	Sequence 51, Appl
44	562	45.6	139	10	US-09-796-692-901	Sequence 901, App
45	562	45.6	139	15	US-10-040-862-901	Sequence 901, App

ALIGNMENTS

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RESULT 1
US-09-948-429B-10
; Sequence 10, Application US/09948429B
; Patent No. US2002017689A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/948,429B
;   FILING DATE:
;   CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
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RESULT 2
US-10-124-807-10
; Sequence 10, Application US/10124807
; Publication No. US2003016620781
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-10

Query Match 100.0%; Score 1232; DB 10; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.6e-90;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
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Qy   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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Db   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy  121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
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Qy  181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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RESULT 3
US-10-291-532-10
; Sequence 10, Application US/10291532
; Publication No. US2003018029081
; GENERAL INFORMATION:
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
; TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
; TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
; FILE REFERENCE: 037003/291872
; CURRENT APPLICATION NUMBER: US/10/291,532
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/331,187
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/758,173
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/383,916
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 08/487,950
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primatized peptide sequence
US-10-291-532-10

Query Match 100.0%; Score 1232; DB 12; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.6e-90;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
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; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:01:50 ; Search time 3758.85 Seconds
                                        (without alignments)
                                        15574.362 Million cell updates/sec

Title: US-09-758-173-11
Perfect score: 1431
Sequence: 1 ATGAAACACCTGTGGTTCTT.........CCCTGTCTCCGGGTAAATGA 1431

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result NO.	Score	% Query Match	Length	DB	ID	Description
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2	1431	100.0	1431	6	AR265201	AR265201 Sequence
3	1429.4	99.9	1431	6	BD063039	BD063039 Identific
4	1315.8	91.9	1431	6	AR108863	AR108863 Sequence
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6	1314.2	91.8	1431	6	BD063035	BD063035 Identific
7	1276.4	89.2	1567	6	AR135359	AR135359 Sequence
8	1261.2	88.1	1431	6	E10697	E10697 cDNA encodi
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15	1181	82.5	1404	6	AR135375	AR135375 Sequence
16	1177.8	82.3	1404	6	AR135377	AR135377 Sequence
17	1176.2	82.2	1404	6	AR135376	AR135376 Sequence
18	1151	80.4	1428	6	BD097232	BD097232 A therape
19	1142.6	79.8	1630	6	BC024289	BC024289 Homo sapi
20	1134.8	79.3	1428	6	AR031184	AR031184 Sequence
21	1134.8	79.3	1428	6	AR042589	AR042589 Sequence
22	1134.8	79.3	1428	6	AR059282	AR059282 Sequence
23	1134.8	79.3	1428	6	AR076260	AR076260 Sequence
24	1134.8	79.3	1428	6	AR300617	AR300617 Sequence
25	1134	79.2	1425	6	AY172959	AY172959 Homo sapi
26	1134	79.2	1430	6	AX419496	AX419496 Sequence
27	1134	79.2	1673	9	HSIGG1LH	Y14737 Homo sapien
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30	1130.6	79.0	1633	9	AK097859	AK097859 Homo sapi
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34	1125.2	78.6	1428	6	AR076262	AR076262 Sequence
35	1125.2	78.6	1428	6	AR300619	AR300619 Sequence
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37	1122.8	78.5	1599	6	AX333307	AX333307 Sequence
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45	1118	78.1	1449	6	BD078407	BD078407 Antigen-b

ALIGNMENTS

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LOCUS   AR108867   1431 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION   Sequence 11 from patent US 6113898.
ACCESSION   AR108867
VERSION   AR108867.1 GI:12825143
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1431)
  AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
  TITLE   Human B7.1-specific primatized antibodies and transfectomas
             expressing said antibodies
  JOURNAL   Patent: US 6113898-A 11 05-SEP-2000; .

Pred. No. is the number of results predicted by chance to have a

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ORIGIN

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Best Local Similarity   100.0%;   Pred. No. 6.2e-277;
Matches 1431;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120
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Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120

Qy  121 TGCGCTGTCTCTGGTGCTCCATCAGCGGTGGTTATGGCTGGTGGGGCTGGGGCTGGGGC  180
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Qy  181 CCAGGGAAGGGGCTGAGTGGATTGGGAGTTCTATAGTAGTAGTGGGAACACCTACTAC  240
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Qy  241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCAAGAACCAGTTCTCC  300
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Db  241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCAAGAACCAGTTCTCC  300

Qy  301 CTGAAGCTGAACTCTATGACCCGCCGACACGGCCGTGTATTACTGTGTGAGAGATCGT  360
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Qy  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
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Qy  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACACATGCCCACCGTGCCCAGCA  780
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Qy  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020
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Qy 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140
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Qy 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1380
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RESULT 2
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LOCUS   AR265201   1431 bp   DNA   linear   PAT 10-APR-2003
DEFINITION   Sequence 11 from patent US 6492134.
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VERSION   AR265201.1   GI:2969362 2
KEYWORDS   .
SOURCE   Unknown.
   ORGANISM   Unknown.
           Unclassified.
REFERENCE   1 (bases 1 to 1431)
   AUTHORS   Aquin,S. and Vezina,Louis.-P.
   TITLE   Method for producing polyhydroxyalkanoates in recombinant organisms
   JOURNAL   Patent: US 6492134-A 11 10-DEC-2002;
FEATURES   Location/Qualifiers
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BASE COUNT   319 a   462 c   385 g   265 t
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OM nucleic - nucleic search, using sw model

Run on:    October  2, 2003, 12:12:30 ; Search time 293.094 Seconds
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Sequence:       1 ATGAAACACCTGGTTCTT.........CCCTGTCTCCGGGTAAATGA 1431

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:       5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1431	100.0	1431	18	AAT62513	Primatised anti-hu
2	1431	100.0	1431	19	AAV35489	Macaque primatized
3	1431	100.0	1431	24	AAS17247	DNA sequence of a
4	1315.8	91.9	1431	18	AAT62510	Primatised anti-hu
5	1315.8	91.9	1431	19	AAV35485	Macaque primatized
6	1315.8	91.9	1431	24	AAS17243	DNA sequence of a
7	1276.4	89.2	1567	22	AAC66522	Human immune syste
8	1261.2	88.1	1431	17	AAT18059	Monoclonal antibod

9	1261	88.1	1634	21	AAZ50012	Human immune syste
10	1224.8	85.6	1418	17	AAT26889	Anti-rhesus D reco
11	1181	82.5	1404	18	AAT62868	Human gamma-4 heav
12	1177.8	82.3	1404	18	AAT62870	Human gamma-4PE he
13	1176.2	82.2	1404	18	AAT62869	Human gamma-4E hea
14	1151	80.4	1428	22	AAH74680	Nucleotide sequenc
15	1151	80.4	1428	25	ABT34317	Hepatitis C virus
16	1136.4	79.4	1428	18	AAT61241	Human anti-RSV mon
17	1134	79.2	1430	24	AAK98701	cDNA of the heavy
18	1134	79.2	1430	25	ABX12855	Human monoclonal r
19	1134	79.2	1544	22	AAS22593	Human cDNA encodin
20	1133.8	79.2	1507	21	AAA09695	Human immunoglobul
21	1133.4	79.2	1798	21	AAC98220	Human colon cancer
22	1123.6	78.5	1428	18	AAT61279	Human anti-RSV mon
23	1122.8	78.5	1599	24	ABK64550	Human benign prost
24	1122.8	78.5	1599	24	ABL62673	Colon adenocarcino
25	1122.8	78.5	1599	24	ABL65479	Lung cancer relate
26	1122.8	78.5	1599	24	ABL66294	Lung cancer relate
27	1120.2	78.4	1617	19	AAQ35099	Antibody D heavy c
28	1120.8	78.3	19035	19	AAV61794	Traget plasmid Man
29	1119.6	78.2	1549	13	AAQ20066	Encodes heavy chai
30	1119	78.1	1442	22	AAC84208	Plasmid Glambda-1B
31	1118	78.1	1449	20	AAX06951	Monoclonal antibod
32	1118	78.1	1449	20	AAX06952	Monoclonal antibod
33	1115.8	78.0	6281	22	AAC84206	Plasmid Glambda-1A
34	1112.4	77.7	1437	19	AAV35487	Macaque primatized
35	1112.4	77.7	1437	24	AAS17245	DNA sequence of a
36	1110.8	77.6	1427	19	AAV41429	Plasmid Hu19BHCpcd
37	1110.8	77.6	1427	19	AAV41431	Plasmid Hu19CHCpcd
38	1110.8	77.6	1437	18	AAT13847	Primatised anti-hu
39	1109.8	77.6	1458	13	AAQ23571	Reshaped CD4 antib
40	1109.8	77.6	1458	13	AAQ23581	Reshaped CD4 antib
41	1109.2	77.5	1427	19	AAV41432	Plasmid Hu19DHCpcd
42	1107.8	77.4	1576	14	AAQ49944	Human anti-HBs hea
43	1107.4	77.4	1416	25	AB224639	Humanised 10D5 ant
44	1104.8	77.2	1392	25	AAD53212	BIWA4/8 antibody h
45	1104.8	77.2	9558	25	AAD53219	BIWA4 antibody DNA

ALIGNMENTS

```
RESULT 1
AAT62513
ID   AAT62513 standard; DNA; 1431 BP.
XX
AC   AAT62513;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis; `
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US10053.
XX
PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
```

```
XX
DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01822.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 11; Fig 10B; 81pp; English.
XX
CC   2 DNA sequences (AAT62512 and AAT62513) respectively code for
CC   primatised forms (AAW01821 and AAW01822) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   16C10.  Cloned 16C10 light and heavy variable genes are inserted
CC   into an expression vector (pref. NEOSPLA) which contains human light
CC   and heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells.  Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

Query Match             100.0%;  Score 1431;  DB 18;  Length 1431;
Best Local Similarity   100.0%;  Pred. No. 6.3e-286;
Matches 1431;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60

Qy     61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

Qy    121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGTGGTGGATCCGGCAGCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGTGGTGGATCCGGCAGCCC 180

Qy    181 CCAGGGAAGGGGCTGGAGTGGCTGGGAGTTTCTATAGTAGTAGTAGTGGAACACCTACTAC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAGGGAAGGGGCTGGAGTGGCTGGGAGTTTCTATAGTAGTAGTAGTGGAACACCTACTAC 240

Qy    241 AACCCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AACCCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300

Qy    301 CTGAAGCTGAACTCTATGACCGCCGCCGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGAAGCTGAACTCTATGACCGCCGCCGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360

Qy    361 CTTTTTCAGTGTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCCGGGAGTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTTTTTCAGTGTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCCGGGAGTC 420

Qy    421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480

Qy    481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540

Qy    541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600

Qy    601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660

Qy    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720

Qy    721 GACAAGAAAGCAGAGCCCAAATCTGTGACAAAACTCACACATCGTGCCCACCGTGCCCAGCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GACAAGAAAGCAGAGCCCAAATCTGTGACAAAACTCACACATCGTGCCCACCGTGCCCAGCA 780

Qy    781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840

Qy    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGACCCT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGACCCT 900

Qy    901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960

Qy    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

Qy   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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```
RESULT 2
AAV35489
ID   AAV35489 standard; DNA; 1431 BP.
XX
AC   AAV35489;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 16C10 heavy chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen;
KW   CD80; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   CD86; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key              Location/Qualifiers
FT   CDS              1..1431
FT                    /tag= a
FT                    /product= 16C10 heavy chain
```

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          GenCore version 5.1.6
     Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:05:20 ; Search time 2366.54 Seconds
                                        (without alignments)
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Title: US-09-758-173-11
Perfect score: 1431
Sequence: 1 ATGAAACACCTGTGGTTCTT.........CCCTGTCTCCGGGTAAATGA 1431

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215223B056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : EST:*
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     4: em_estmu:*
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     7: em_estro:*
     8: em_htc:*
     9: gb_est1:*
    10: em_est2:*
    11: gb_htc:*
    12: gb_est3:*
    13: gb_est4:*
    14: gb_est5:*
    15: em_estfun:*
    16: em_estom:*
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    19: em_gss_pln:*
    20: em_gss_vrt:*
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    26: em_gss_phg:*
    27: em_gss_vrl:*
    28: gb_gss1:*
    29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
c 1	944	66.0	1201	13	BX377695	BX377695 BX377695
c 2	929.6	65.0	1142	13	BX414495	BX414495 BX414495
c 3	902	63.0	1020	12	BQ062878	BQ062878 AGENCOURT
c 4	899.2	62.8	1045	:13	BX337477	BX337477 BX337477
c 5	894.8	62.5	1149	13	BX381020	BX381020 BX381020
c 6	892.6	62.4	1201	13	BX377803	BX377803 BX377803
c 7	891.2	62.3	1201	13	BX439438	BX439438 BX439438
c 8	889.8	62.2	902	13	BU146962	BU146962 AGENCOURT
c 9	875.8	61.2	1013	13	BX360518	BX360518 BX360518
c 10	867.6	60.6	1200	13	BX415883	BX415883 BX415883
c 11	864	60.4	947	13	BQ709771	BQ709771 AGENCOURT
c 12	850.4	59.4	958	13	BQ706140	BQ706140 AGENCOURT
c 13	849.2	59.3	1093	13	BX428863	BX428863 BX428863
c 14	842.4	58.9	926	10	BG755166	BG755166 602711488
c 15	835.2	58.4	1096	13	BX415920	BX415920 BX415920
c 16	832	58.1	988	13	BQ708857	BQ708857 AGENCOURT
c 17	831.8	58.1	1201	13	BX338493	BX338493 BX338493
c 18	831.2	58.1	901	12	BM007892	BM007892 503617577
c 19	830.6	58.0	985	13	BX457369	BX457369 BX457369
c 20	829.4	57.6	1201	13	BX417147	BX417147 BX417147
c 21	824.4	57.5	1029	13	BQ063185	BQ063185 AGENCOURT
c 22	823.2	57.5	1019	13	BX325650	BX325650 BX325650
c 23	822.8	57.5	887	13	BQ711255	BQ711255 AGENCOURT
c 24	822.0	57.5	918	13	BQ708022	BQ708022 AGENCOURT
c 25	818.6	57.2	995	12	BM914540	BM914540 AGENCOURT
c 26	818	57.2	1015	13	BX367600	BX367600 BX367600
c 27	817.8	57.1	980	13	BX325701	BX325701 BX325701
c 28	811.8	56.7	889	13	BX346909	BX346909 BX346909
c 29	811	56.7	1147	13	BX360330	BX360330 BX360330
c 30	809	56.5	1009	13	BX456658	BX456658 BX456658
c 31	808.8	56.5	881	13	BQ711291	BQ711291 AGENCOURT
c 32	807.4	56.4	1200	13	BX456326	BX456326 BX456326
c 33	804	56.2	853	13	BX388631	BX388631 BX388631
c 34	801.6	56.0	862	13	BX450248	BX450248 BX450248
c 35	800.2	55.9	1031	13	BQ064886	BQ064886 AGENCOURT
c 36	799.4	55.9	852	13	BX450232	BX450232 BX450232
c 37	798.4	55.8	1004	13	BX432300	BX432300 BX432300
c 38	797.4	55.7	936	13	BQ711727	BQ711727 AGENCOURT
c 39	796	55.6	940	13	BQ705928	BQ705928 AGENCOURT
c 40	795.6	55.6	1070	13	BX397632	BX397632 BX397632
c 41	795.2	55.6	1152	13	BX339318	BX339318 BX339318
c 42	794.8	55.5	1201	13	BX380759	BX380759 BX380759
c 43	794.2	55.5	1151	13	BX378450	BX378450 BX378450
c 44	792.2	55.4	885	13	BX408117	BX408117 BX408117
c 45	791.2	55.3	1201	13	BX396322	BX396322 BX396322

ALIGNMENTS

RESULT 1
BX377695/c
LOCUS   BX377695   1201 bp   mRNA   linear   EST 08-MAY-2003
DEFINITION BX377695 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI009vJ10 3-PRIME, mRNA sequence.
ACCESSION   BX377695
VERSION   BX377695.1 GI:30439018
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI009DE05NPI&cluster=7198.r. Contact :
            Feng Liang Email: fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

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FEATURES         Faraday Avenue Genoscope sequence ID : CS0DI009DE05NP1.
     source      Location/Qualifiers
                 1..1201
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="CS0DI009YJ10"
                 /tissue_type="PLACENTA COT 25-NORMALIZED"
                 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                 /note="1st strand cDNA was primed with a NotI-oligo(dT)
                 primer. Five prime end enriched, double-strand cDNA was
                 digested with Not I and cloned into the Not I and EcoR V
                 sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT     188 a     296 c     396 g     267 t     54 others
ORIGIN

Query Match         66.08;   Score 944;   DB 13;   Length 1201;
Best Local Similarity  95.88;   Pred. No. 4e-215;
Matches  991;  Conservative  17;  Mismatches  22;  Indels  4;  Gaps  4;
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```
Qy     398  TCGATGTCGGGGGCCCCGGAGTCCTGGTCACCGTTCCTCAGCTAGCACCAAGGGCCCAT  457
                  |||||||||| ||||||| ||||| |  || : | : | |||||||||||||
Db    1119  TTKACWACTGGGGCCAAGGAHCTTTGTTCACCGTCCYTCAGCYTCAACCAAGGGCCCAT 1060

Qy     458  CGGTCTCCCCCTGGCACCTTCTCCAAGAGCACCTTCGGGGCACCAGCCGCCCTGGGCT  517
                 ||||| :|||||  |||||||||||||||||||| : ||||||||||:||||||
Db    1059  CGGTYTYCCCC-KGCACACCTTCTCCAAGAGCACCTTCGGGGCSCCCTGGGCT 1001

Qy     518  GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGA  577
                 ||||||||||||||||||||||||||| : |||||||||||||||||||||||||
Db    1000  GCCTKGTCAAGGACTACTTCCCCGAACC-GTGACGGTGTCGTGGAACTCAGGCGCCCTGA  942

Qy     578  CCAGCGGCGTGCACACCTTCCCGGCTGTCCTCACGGCTCCTCAGGACTCCTCACCTCCTCAGCA  637
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Db     941  CCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGWCCTCAGGACTCTACTTCCCTCAGCA  882

Qy     638  GGCTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGCACCTACATCTGCAAGTGAATC  697
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Db     881  GCGTGGTGACCGTGCCCTCCAGCAGCGTKG-GCACCCAGCACCTACATCTGCAAGTGAATC  823

Qy     698  ACAAGGCCAGCAACAACAAGGTGGACAAGAAAGCAGCCCAAATCTTGTGACAAAACTC  757
                 |||||||||||||||||||||||||| |  || ||||||| ||||||||||||||
Db     822  ACAAGGCCAGCAACAACAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTC  763

Qy     758  ACACATGCCCACCGTGCCCAGCACCTGAACTCTGGGGGACCGTCAGTCTTCCTCTTCC  817
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Qy     818  CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACAATGCGTGGTGG  877
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Qy     878  TGGACGTGAGCCAGGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG  937
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Qy     938  TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA  997
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Qy     998  GGGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 1057
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REFERENCE   1  (bases 1 to 1142)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0CAP001AE07NP1&cluster=7198.r. Contact :
            Feng Liang Email : fliang@lifetech.com
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0CAP001AE07NP1.
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            /note="vector: pCMVSPORT_6; 1st strand cDNA was primed
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            double-strand cDNA was digested with Not I and cloned into
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            Library was not normalized."
BASE COUNT   193 a    290 c    381 g    251 t    27 others
ORIGIN

Query Match         65.08;   Score 929.6;  DB 13;  Length 1142;
Best Local Similarity  98.2%;  Pred. No. 1.1e-211;
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Db    1078  TTTCCCCTTGGACCCCTCCTCCAAAGAGMACTTCTGGGGG-AMAGCGCCCGGGGGCCCTG 1020

Qy     523  GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC  582
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Db     523  GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC  582
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:10:05 ; Search time 76.0531 Seconds
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Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1431	100.0	1431	3	US-09-526-098-11	Sequence 11, Appl
3	1315.8	91.9	1431	3	US-08-487-550-3	Sequence 3, Appli
4	1315.8	91.9	1431	4	US-09-526-098-3	Sequence 3, Appli
5	1276.4	89.2	1567	4	US-09-049-672A-17	Sequence 17, Appli
6	1213.6	84.8	1418	4	US-08-793-450-7	Sequence 7, Appli
7	1181	82.5	1404	3	US-08-523-894-7	Sequence 7, Appli
8	1177.8	82.3	1404	3	US-08-523-894-11	Sequence 11, Appli
9	1176.2	82.2	1404	3	US-08-523-894-9	Sequence 9, Appli
10	1134.8	79.3	1428	1	US-08-488-376-17	Sequence 17, Appli
11	1134.8	79.3	1428	2	US-08-634-223-17	Sequence 17, Appli
12	1134.8	79.3	1428	2	US-08-634-224-17	Sequence 17, Appl
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21	1125.2	78.6	1428	2	US-08-634-400-19	Sequence 19, Appl
22	1125.2	78.6	1428	2	US-08-635-878-19	Sequence 19, Appl
23	1125.2	78.6	1428	2	US-08-770-057-19	Sequence 19, Appl
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25	1125.2	78.6	1428	4	US-09-740-002-19	Sequence 19, Appl
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29	1118	78.1	19040	4	US-09-343-485A-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 11, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
   APPLICANT: Anderson, Darrell R.
   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
   NUMBER OF SEQUENCES: 12
   CORRESPONDENCE ADDRESS:
     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
     STREET: 699 Prince Street
     CITY: Alexandria
     STATE: VA
     COUNTRY: USA
     ZIP: 22314
   COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
     SOFTWARE: PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/08/487,550
     FILING DATE: 07-JUN-1995
     CLASSIFICATION: 435
   ATTORNEY/AGENT INFORMATION:
     NAME: Teskin, Robin L.
     REGISTRATION NUMBER: 35,030
     REFERENCE/DOCKET NUMBER: 012712-131
   TELECOMMUNICATION INFORMATION:
     TELEPHONE: 703-836-6620
     TELEFAX: 703-836-2021
   INFORMATION FOR SEQ ID NO: 11:
   SEQUENCE CHARACTERISTICS:
     LENGTH: 1431 base pairs
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     STRANDEDNESS: not relevant
     TOPOLOGY: linear
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US-08-487-550-11

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Best Local Similarity 100.0%; Pred. No. 0:
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October  2, 2003, 19:53:01 ; Search time 283.087 Seconds
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Perfect score: 1431
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Searched:    1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters:    3416838

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
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3	1431	100.0	1431	12	US-10-291-532-11	Sequence 11, Appl
4	1431	100.0	1431	13	US-10-124-905-11	Sequence 11, Appl
5	1429.4	99.9	1431	13	US-10-073-138-6	Sequence 6, Appli
6	1315.8	91.9	1431	10	US-09-948-429B-3	Sequence 3, Appli
7	1315.8	91.9	1431	12	US-10-124-807-3	Sequence 3, Appli
8	1315.8	91.9	1431	12	US-10-291-532-3	Sequence 3, Appli
9	1315.8	91.9	1431	13	US-10-124-905-3	Sequence 3, Appli
10	1314.2	91.8	1431	13	US-10-073-138-2	Sequence 2, Appli
11	1181	82.5	1404	14	US-10-211-357-7	Sequence 7, Appli
12	1177.8	82.3	1404	14	US-10-211-357-11	Sequence 11, Appli
13	1176.2	82.2	1404	14	US-10-211-357-9	Sequence 9, Appli
14	1151	80.4	1428	12	US-10-203-754A-40	Sequence 40, Appli
15	1134.8	79.3	1428	9	US-09-740-002-17	Sequence 17, Appl
16	1134	79.2	1430	12	US-10-225-108A-1	Sequence 1, Appli
17		79.2	1134	12	US-09-848-832-1	Sequence 1, Appli
18		79.2	1133.4	9	US-09-925-299-230	Sequence 230, App
19		79.2	1133.4	9	US-09-925-299-230	Sequence 230, App
20		78.6	1125.2	11	US-09-740-002-19	Sequence 19, Appl
21		78.5	1122.8	10	US-09-954-456-789	Sequence 789, App
22		78.5	1122.8	12	US-09-954-456-1604	Sequence 1604, Ap
23		78.5	1122.8	12	US-09-873-319-445	Sequence 445, App
24		78.5	1122.8	12	US-09-960-706-704	Sequence 704, App
25		78.5	1122.8	9	US-09-873-367C-1010	Sequence 1010, Ap
26		78.1	1118	12	US-10-225-108A-15	Sequence 15, Appl
27		78.1	1118	10	US-09-747-669-1	Sequence 1, Appli
28 c		78.1	1118	10	US-09-747-669-2	Sequence 2, Appli
29		78.1	1118	14	US-10-290-703-1	Sequence 1, Appli
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31		77.7	1112.4	10	US-09-948-429B-7	Sequence 7, Appli
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33		77.7	1112.4	12	US-10-291-532-7	Sequence 7, Appli
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35		77.7	1112.4	13	US-10-073-138-4	Sequence 4, Appli
36		77.6	1110.8	13	US-10-066-895-20	Sequence 20, Appli
37		77.5	1110.8	13	US-10-066-895-25	Sequence 25, Appli
38		77.5	1109.2	13	US-10-066-895-27	Sequence 27, Appli
39		77.2	1104.8	13	US-10-150-475A-7	Sequence 7, Appli
40		77.1	1102.8	13	US-10-066-895-14	Sequence 14, Appl
41		76.9	1100.4	10	US-09-822-698A-27	Sequence 27, Appl
42		76.9	1100	9	US-09-822-849A-87	Sequence 87, Appl
43		76.7	1098.2	10	US-09-822-830A-571	Sequence 571, App
44		76.6	1096.6	11	US-09-911-692-3	Sequence 3, Appli
45		76.6	1096.6	10	US-09-911-703-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT 1
US-09-948-429B-11
; Sequence 11, Application US/09948429B
; Patent No. US2002017768A1
GENERAL INFORMATION:
  APPLICANT: Anderson, Darrell R.
  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
  TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
  NUMBER OF SEQUENCES: 12
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
    STREET: 699 Prince Street
    CITY: Alexandria
    STATE: VA
    COUNTRY: USA
    ZIP: 22314
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09-948,429B
    FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/383,916
    FILING DATE:
    APPLICATION NUMBER: US 08/487,550
    FILING DATE: 07-JUN-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: Teskin, Robin L.
    REGISTRATION NUMBER: 35,030
    REFERENCE/DOCKET NUMBER: 012712-131
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 703-836-6620
    TELEFAX: 703-836-2021
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; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1431 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: not relevant
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..1431
;   FEATURE:
;     NAME/KEY: mat_peptide
;     LOCATION: 1..1431
US-09-948-429B-11

  Query Match         100.0%;  Score 1431;  DB 10;  Length 1431;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360
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Qy    781 CCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
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Qy    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTGCACGTCCTGCACCAG 1020
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  2, 2003, 08:56:23 ; Search time 55.856 Seconds
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Title:      US-09-758-173-12
Perfect score: 2549
Sequence:   1 MKHLWFFLLLVAAPRWVLSQ........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:   1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:    1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2549	100.0	476	18	AAW01822	Primatised anti-hu
2	2549	100.0	476	19	AAW63765	Macaque primatized
3	2549	100.0	476	23	AAU11646	Protein sequence o
4	2342.5	91.9	473	22	AAB36206	Human immune syste
5	2309	90.6	476	18	AAW01818	Primatised anti-hu
6	2309	90.6	476	19	AAW63761	Macaque primatized
7	2309	90.6	476	23	AAU11539	Protein sequence o
8	2296.5	90.1	475	17	AAR93553	Monoclonal antibod
9	2278	89.4	470	21	AAY44721	Human immune syste
10	2217	87.0	472	17	AAR93166	Anti-rhesus D reco
11	2206	86.5	453	24	ABP96295	4A5-3.1-B4 antib
12	2162.5	84.8	467	13	AAR22759	Reshaped CD4 antib
13	2159.5	84.7	467	13	AAR22758	Reshaped CD4 antib
14	2148	84.3	470	13	AAR22757	Reshaped CAMPATH-1
15	2145.5	84.2	467	18	AAW14927	Human gamma-4PE he
16	2144.5	84.1	467	18	AAW14925	Human gamma-4 heav
17	2138.5	83.9	446	18	AAW05829	Humanised 1D10 ant
18	2137.5	83.9	467	18	AAW14926	Human gamma-4E hea
19	2134.5	83.7	581	22	AAB81972	Ganglioside GD2 sp
20	2126.5	83.4	475	18	AAW11639	Human anti-RSV mon
21	2126.5	83.4	475	22	AAG63640	Amino acid sequenc
22	2126	83.4	451	20	AAY50031	Human E27 anti-IgE
23	2126	83.4	451	20	AAW95663	Mus musculus anti-
24	2126	83.4	451	21	AAB07473	Amino acid sequenc
25	2126	83.4	451	22	AAB74212	E27 anti-IgE antib
26	2126	83.4	451	22	AAB76952	Full length heavy
27	2124	83.3	451	20	AAW95659	Mus musculus anti-
28	2124	83.3	451	20	AAW95661	Mus musculus anti-
29	2124	83.3	451	21	AAY85201	Light chain amino
30	2124	83.3	451	21	AAB47088	Anti-IgE antibody,
31	2124	83.3	451	22	AAB76948	Full length heavy
32	2124	83.3	451	22	AAB76950	Full length heavy
33	2122.5	83.3	450	22	AAE10515	Humanised high pot
34	2122.5	83.3	450	23	ABP66572	Human RSV antibody
35	2122.5	83.3	450	23	ABP66604	Human RSV antibody
36	2122.5	83.3	450	24	ABU69435	Respiratory syncyt
37	2122.5	83.2	450	24	ABU69467	Respiratory syncyt
38	2121	83.2	462	21	AAB26884	Human immunoglobul
39	2120.5	83.2	450	22	AAE10521	Humanised high pot
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41	2120.5	83.2	450	24	ABU69433	Respiratory syncyt
42	2120.5	83.2	472	24	ABP58289	Humanised 1OD5 ant
43	2119.5	83.2	450	22	AAE10511	Humanised high pot
44	2119.5	83.2	450	22	AAE10513	Humanised high pot
45	2119.5	83.2	450	23	ABP66576	Human RSV antibody

ALIGNMENTS

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RESULT 1
AAW01822
ID   AAW01822 standard; Protein;  476 AA.
XX
AC   AAW01822;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US10053.
XX
PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
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DR   WPI; 1997-108538/10.
DR   N-PSDB: AAT62513.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 14; Fig 10B; 81pp; English.
XX
CC   2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
CC   heavy variable genes (see also AAT62512 and AAT62513) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20). The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence   476 AA;

Query Match   100.0%;   Score 2549;   DB 18;   Length 476;
Best Local Similarity 100.0%;   Pred. No. 5.8e-149;
Matches 476;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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Qy   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
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Db   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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Db   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy   301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

Qy   361 IEKTISKAKGQPREPQVYTLPPSRDELKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IEKTISKAKGQPREPQVYTLPPSRDELKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Qy   421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476

RESULT 2
AAW63765
ID   AAW63765 standard; Protein; 476 AA.
XX
AC   AAW63765;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 16C10 heavy chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;

KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US19906.
XX
PR   08-NOV-1996;   96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB: AAV35489.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 5b; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 16C10 heavy
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAB's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAB can be conjugated to a drug or toxin. MAB's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAB's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence   476 AA;

Query Match   100.0%;   Score 2549;   DB 19;   Length 476;
Best Local Similarity 100.0%;   Pred. No. 5.8e-149;
Matches 476;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSERLSLTCAVSGGSISGGYGWGWIRQP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120

Qy   121 LFSVVGMYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LFSVVGMYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

Qy   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy   301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  2, 2003, 08:56:23 ; Search time 13.1295 Seconds
                                        (without alignments)
                                        1704.917 Million cell updates/sec

Title:     US-09-758-173-12
Perfect score: 2549
Sequence:  1 MKHLWFFLLLVAAPRWVLSQ........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:      127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     SwissProt_41:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

Result          %    Query
 No.   Score  Match Length DB ID            Description
-----  -----  ----- ------ -- --            -----------
   1   1763   69.2   330   1  GC1_HUMAN     P01857 homo sapien
   2   1600   62.8   326   1  GC2_HUMAN     P01859 homo sapien
   3  1586.5  62.2   327   1  GC4_HUMAN     P01861 homo sapien
   4  1226.5  48.1   323   1  GC_RABIT      P01870 oryctolagus
   5  1212.5  47.6   329   1  GC2_CAVPO     P01862 cavia porce
   6   1157   45.4   290   1  GC3_HUMAN     P01860 homo sapien
   7   1148   45.0   326   1  GC1_RAT       P20759 rattus norv
   8  1142.5  44.8   333   1  GCB_RAT       P20761 rattus norv
   9   1138   44.6   324   1  GC1_MOUSE     P01868 mus musculu
  10   1137   44.6   329   1  GC3_MOUSE     P22436 mus musculu
  11   1133   44.4   393   1  GC1M_MOUSE    P01869 mus musculu
  12   1126   44.2   398   1  GC3M_MOUSE    P03987 mus musculu
  13   1122   44.0   330   1  GCAA_MOUSE    P01863 mus musculu
  14  1119.5  43.9   335   1  GCAB_MOUSE    P01864 mus musculu
  15   1117   43.8   399   1  GCAM_MOUSE    P01865 mus musculu
  16  1114.5  43.7   329   1  GCC_RAT       P20762 rattus norv
  17   1108   43.5   322   1  GCA_RAT       P20760 rattus norv
  18   1085   42.6   336   1  GCB_MOUSE     P01866 mus musculu
  19   1080   42.4   405   1  GCBM_MOUSE    P01867 mus musculu
  20    489   19.2   428   1  EPC_HUMAN     P01854 homo sapien
  21  483.5   19.0   429   1  EPC_RAT       P06336 rattus norv
  22    465   18.2   421   1  EPC_MOUSE     P06331 homo sapien
  23    458   18.0   146   1  HV21_HUMAN    P01871 homo sapien
  24    442   17.3   454   1  MUC_HUMAN     P03988 oryctolagus
  25    437   17.1   458   1  MUC_RABIT     P01872 mus musculu
  26  432.5   17.0   455   1  MUC_MOUSE     P04221 oryctolagus
  27    427   16.8   479   1  MUCM_RABIT    P20768 suncus muri
  28    425   16.7   457   1  MUC_SUNMU     P01873 mus musculu
  29  422.5   16.6   476   1  MUCM_MOUSE    P01824 homo sapien
  30    420   16.5   129   1  HV2F_HUMAN    P01874 canis famil
  31    420   16.5   450   1  MUC_CANFA     P06337 mesocricetu
  32  415.5   16.3   454   1  MUC_MESAU     P04220 homo sapien
  33    403   15.8   391   1  MUCB_HUMAN
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  34   396.5  15.6   137   1  HV46_MOUSE    P01822 mus musculu
  35  395.5   15.5   438   1  HVC2_HETFR    P23085 heterodontu
  36    394   15.5   438   1  HVCS_HETFR    P23087 heterodontu
  37    385   15.1   461   1  HVCM_HETFR    P23088 heterodontu
  38    384   15.1   370   1  HVC1_HETFR    P23084 heterodontu
  39  383.5   15.0   353   1  ALC1_HUMAN    P01876 homo sapien
  40  380.5   14.9   353   1  ALC1_GORGO    P20758 gorilla gor
  41    379   14.9   340   1  ALC2_HUMAN    P01877 homo sapien
  42    368   14.4   116   1  HV60_MOUSE    P18531 mus musculu
  43  366.5   14.4   393   1  HV3_HETFR     P23086 heterodontu
  44    362   14.2   117   1  HV2G_HUMAN    P01825 homo sapien
  45    361   14.2   116   1  HV61_MOUSE    P18532 mus musculu
```

```
                              ALIGNMENTS

RESULT 1
GC1_HUMAN
ID   GC1_HUMAN      STANDARD;      PRT;    330 AA.
AC   P01857;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-1 chain C region.
GN   IGHG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82274238; PubMed=6287432;
RA   Ellison J.W., Berson B.J., Hood L.E.;
RT   "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL   Nucleic Acids Res. 10:4071-4079(1982).
RN   [2]
RP   SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [3]
RP   SEQUENCE OF 136-329 (EU).
RX   MEDLINE=71064025; PubMed=5530842;
RA   Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA   Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL   Biochemistry 9:3171-3181(1970).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN NIE).
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [5]
RP   SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6684994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
```

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RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981)
CC   -!- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
CC       G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
CC       MARKER & THE G1M (NON-1) MARKERS.
CC   -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC       35,116,198,269 & 272.
CC   -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC       155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC       268-272.
CC   -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC       RESIDUES 198,267&272.
CC   --------------------------------------------------------------------------
CC   This SWIS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GHHU.
DR   PDB; 1FC1; 15-JUL-92.
DR   PDB; 1FC2; 15-JUL-92.
DR   PDB; 1AJ7; 12-NOV-97.
DR   PDB; 1D5B; 09-FEB-00.
DR   PDB; 1D5I; 09-FEB-00.
DR   PDB; 1D6V; 04-OCT-00.
DR   PDB; 1DN2; 17-MAY-00.
DR   PDB; 1E4K; 06-JUN-01.
DR   PDB; 1FCC; 20-JUL-95.
DR   PDB; 1HZH; 12-JUN-02.
DR   PDB; 1I7Z; 08-AUG-01.
DR   PDB; 1IIS; 16-MAY-01.
DR   PDB; 1IIX; 16-MAY-01.
DR   PDB; 1L6X; 10-APR-02.
DR   PDB; 2RCS; 12-NOV-97.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100;
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       INTERCHAIN (WITH LIGHT CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    144    204
FT   CARBOHYD    180    180       N-LINKED (GLCNAC...).
FT   MOD_RES     330    330       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT      97     97       K -> R (IN G1M(3) MARKER).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003888.
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    147
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    166
FT   TURN        168    171
FT   STRAND      176    179
FT   TURN        180    181
FT   STRAND      182    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      260    265
FT   STRAND      270    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      305    312
FT   TURN        313    314
FT   TURN        316    317
FT   STRAND      320    325
SQ   SEQUENCE    330 AA;  36106 MW;  3770EE106C2FA33D CRC64;

Query Match    69.2%;
Best Local Similarity   99.7%;   Score 1763;  DB 1;  Length 330;
Matches  329;  Conservative   0;  Mismatches   1;  Pred. NO. 6.5e-114;
                                                   Indels   1;  Gaps   0;

Qy   147  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  206
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS   60

Qy   207  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG  266
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    61  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLGG  120

Qy   267  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN  326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN  180

Qy   327  STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE  386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE  240

Qy   387  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  446
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  300
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                 GenCore version 5.1.6
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     October  2, 2003, 08:56:23 ; Search time 46.0645 Seconds
                                          (without alignments)
                                          2666.544 Million cell updates/sec

Title:      US-09-758-173-12
Perfect score: 2549
Sequence:   1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:   830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:     830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SPTREMBL_23:*
            1: sp_archea:*
            2: sp_bacteria:*
            3: sp_fungi:*
            4: sp_human:*
            5: sp_invertebrate:*
            6: sp_mammal:*
            7: sp_mhc:*
            8: sp_organelle:*
            9: sp_phage:*
           10: sp_plant:*
           11: sp_rodent:*
           12: sp_virus:*
           13: sp_vertebrate:*
           14: sp_unclassified:*
           15: sp_rvirus:*
           16: sp_bacteriap:*
           17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2102.5	82.5	471	4	Q8TC77	Q8tc77 homo sapien
2	2075	81.4	473	4	Q8TC63	Q8tc63 homo sapien
3	1927.5	75.6	521	4	Q8N4Y9	Q8n4y9 homo sapien
4	1612.5	63.3	509	4	Q8NF17	Q8nf17 homo sapien
5	1473.5	57.8	463	11	Q99LC4	Q99lc4 mus musculu
6	1437.5	56.4	473	11	Q9D8L4	Q9d8l4 mus musculu
7	1434	56.3	469	11	Q8R3V9	Q8r3v9 mus musculu
8	1430.5	56.1	437	11	Q9R1A4	Q9r1a4 mus musculu
9	1416	55.6	468	11	Q99L31	Q99l31 mus musculu
10	1394.5	54.7	473	11	Q99L25	Q99l25 mus musculu
11	1367	53.6	474	11	Q8R3H6	Q8r3h6 mus musculu
12	1365.5	53.6	473	11	Q91Z05	Q91z05 mus musculu
13	1268	49.7	701	4	Q96PQ8	Q96pq8 homo sapien
14	1262.5	49.5	337	6	Q95M34	Q95m34 equus cabal
15	973	38.2	613	4	Q96EY0	Q96ey0 homo sapien
16	948.5	37.2	597	4	Q9BU10	Q9bu10 homo sapien
17	944.5	37.1	597	4	Q9BQB8	Q9bqb8 homo sapien
18	938.5	36.8	588	4	Q8WUX4	Q8wux4 homo sapien
19	933.5	36.8	618	4	Q96AA6	Q96aa6 homo sapien
20	915	35.9	496	4	Q96KX8	Q96kx8 homo sapien
21	770.5	30.2	597	4	Q96BB9	Q96bb9 homo sapien
22	762	29.9	613	4	Q8WUK1	Q8wuk1 homo sapien
23	746.5	29.3	479	11	Q99M22	Q99m22 mus musculu
24	726	28.5	613	11	Q8VCX7	Q8vcx7 mus musculu
25	725	28.4	278	11	Q921K1	Q921k1 mus musculu
26	702	27.5	494	4	Q95K68	Q95k68 homo sapien
27	700	27.5	482	11	Q91X92	Q91x92 mus musculu
28	692.5	27.2	493	4	Q8NCL6	Q8ncl6 homo sapien
29	692.5	27.2	614	4	Q96GA6	Q96ga6 homo sapien
30	687.5	27.0	499	4	Q8N5K4	Q8n5k4 homo sapien
31	667.5	26.2	497	4	Q8WY24	Q8wy24 homo sapien
32	655.5	25.7	479	11	Q91WP5	Q91wp5 mus musculu
33	655	25.7	488	11	Q91WR1	Q91wr1 mus musculu
34	654.5	25.7	487	11	Q99KA4	Q99ka4 mus musculu
35	652	25.6	486	11	Q91Z07	Q91z07 mus musculu
36	645	25.3	500	4	Q9BRV0	Q9brv0 homo sapien
37	637.5	25.0	481	11	Q91WT1	Q91wt1 mus musculu
38	636	25.0	496	4	Q96DK0	Q96dk0 homo sapien
39	635.5	24.9	481	11	Q8VCV5	Q8vcv5 mus musculu
40	631.5	24.8	480	11	Q91XE1	Q91xe1 mus musculu
41	629	24.7	482	11	Q8K172	Q8k172 mus musculu
42	628	24.6	488	11	Q8K0F2	Q8k0f2 mus musculu
43	626.5	24.6	489	11	Q8VCX4	Q8vcx4 mus musculu
44	623.5	24.5	484	11	Q8VEA0	Q8vea0 mus musculu
45	620	24.3	480	11	Q8K0Z4	Q8k0z4 mus musculu

ALIGNMENTS

```
RESULT 1
Q8TC77
ID   Q8TC77         PRELIMINARY;      PRT;    471 AA.
AC   Q8TC77;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024289; AAH24289.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 4.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE 471 AA;  51791 MW;  38F7F4CF588660E CRC64;

Query Match           82.5%;  Score 2102.5;  DB 4;  Length 471;
Best Local Similarity 85.2%;  Pred. No. 9.9e-162;
Matches 403;  Conservative 16;  Mismatches 45;  Indels 9;  Gaps 4;

Qy      5 WFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSITCAVSGGSISGGYGWGWIRQPPGKG 64
            | ||  ||||  | :|||  |||| |||| .: | |||  :| |||  : ||| ||||
Db      7 WVF--LVAILESVQCEVQLVESGGGLVKPGGSLRLSCAASGFTFS-SYSMNWVRQAPGKG 63

Qy     65 LEWIGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTADTAVYYCVRDRLFSV 124
           |||| || ||  :| ||||||||   | | :| | | || || |||||||  | | |||
Db     64 LEWVSSMSSSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD----- 118
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Db  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTK 239
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy  240 VDKKAAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
        ||||: | |||||    | :  |||||||||||||||||||||||||||||||||||||||
Db  240 VDKRVESK---YGPPCPSCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQED 296

Qy  300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
        |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  297 PEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS 356

Qy  360 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
        |||||||||||||||||||||||||||||:|:||||||||||||||||||||||||||||
Db  357 SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 416

Qy  420 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  417 YKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 473
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RESULT 3

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Q8N4Y9
ID   Q8N4Y9      PRELIMINARY;      PRT;    521 AA.
AC   Q8N4Y9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells from Tonsils;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033178; AAH33178.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE  521 AA;  57156 MW;  2AC7D22E72D6CAA2 CRC64;

Query Match              75.6%;  Score 1927.5; DB 4;  Length 521;
Best Local Similarity    72.4%;  Pred. No. 1.6e-147;
Matches  376;  Conservative   32;  Mismatches  58;  Indels  53;  Gaps  5;

Qy    7 FLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLE 66
          ::|| |||||  |||:|| |||||||    :|||||||::||  |  ||  ||| |||  |
Db    7 WVLLVFLQGVQCEVQLVDSGGGLVQPGGGLRLSCAASGFIVSDHY-VEWVRQAPGKGPE 65

Qy   67 WIGSFYSSS--GNTYINPSLKSQVTISDTISKNQFSLKLNSMTAADTAVYYCVRDRLFSV 124
          | |||||:  |||| |||:||||  :  :| |  ::|::| :  || |||||||||   |
Db   66 WGCFRSKAHKSTTEYAASVKGRFTILRDDSKNSVHLQMNSLKTDDTAVYYCVRD- LEG 123

Qy  125 VGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 184
        |: : ||| ||||||:|||||:|||||||||||||||||||||||||||||||||||||||
Db  124 AGK-YDWYFDIWGRGILVTVSSASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVT 182

Qy  185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYICNVNHKPSNTKVDKKA 244
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  183 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYTCNVNHKPSNTKVDKRV 242

Qy  245 ---------------------------------------------------EPKSCDKTHTCPP 257
                                                              :: |:
Db  243 ELKTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPR 302
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RESULT 2
Q8TC63
ID   Q8TC63      PRELIMINARY;      PRT;    473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE  473 AA;  51986 MW;  E29920B09BA365F5 CRC64;

Query Match              81.4%;  Score 2075; DB 4;  Length 473;
Best Local Similarity    83.2%;  Pred. No. 1.7e-159;
Matches  397;  Conservative   29;  Mismatches  39;  Indels  12;  Gaps  5;

Qy    1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSI-SGGYGWGWIRQ 59
        |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    8 MKHLWFFLLLVAAPRWVLSRLQLQESGPGLLKPSVTLSLTCVSGDSVASSSYYWGWVRQ 67

Qy   60 PPGKGLEWIGSFYSSSGNTYINPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRD 119
        |||||||||||  ::||||    : ||:|:  :::| |  :|::|  |  || ||||||:
Db   68 PPGKGLEWIGTI-NFSGNMYYSPSLRSRVTMSADMSENSFYLKLDSVTAADTAVYYCAAG 126

Qy  120 RLFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
        : | :|:: ||| |:|  ||   ||:|||||||||||:||:|||||| ||||||||||||
Db  127 HL--VMGFGAH----WQQGKLVSVSPASTKGPSVFPLAPCSRSTSSSTAALGCLVKDYF 179

Qy  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYICNVNHKPSNTK 239
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  184 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYICNVNHKPSNTKVDKK 243

Qy  244 AEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 303
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  239 VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 298

Qy  304 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 363
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  299 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 358

Qy  364 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 423
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  359 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 418

Qy  424 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  419 PPVLDSDGSFFLYSRLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:       October  2, 2003, 09:12:09 ; Search time 21.1407 Seconds
                                            (without alignments)
                                            952.562 Million cell updates/sec

Title:        US-09-758-173-12
Perfect score: 2549
Sequence:     1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:     328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:    328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database  :   Issued_Patents_AA:*
          1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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          3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
          4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
          5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	2549	100.0	476	3	US-08-487-550-12	Sequence 12, Appli
2	2549	100.0	476	3	US-09-526-098-12	Sequence 12, Appli
3	2342.5	91.9	473	3	US-09-049-672A-4	Sequence 4, Appli
4	2309	90.6	476	4	US-08-487-550-4	Sequence 4, Appli
5	2309	90.6	476	4	US-09-526-098-4	Sequence 4, Appli
6	2200	86.3	472	4	US-08-793-450-8	Sequence 8, Appli
7	2153.5	84.5	446	3	US-08-397-411-7	Sequence 7, Appli
8	2145.5	84.2	467	3	US-08-523-894-12	Sequence 12, Appli
9	2144.5	84.1	467	3	US-08-523-894-8	Sequence 8, Appli
10	2137.5	83.9	467	2	US-08-887-352B-10	Sequence 10, Appli
11	2126	83.4	451	3	US-09-109-207C-18	Sequence 18, Appli
12	2126	83.4	451	3	US-09-282-505-2	Sequence 2, Appli
13	2126	83.4	451	3	US-09-054-255-2	Sequence 2, Appli
14	2126	83.4	451	4	US-09-296-005-18	Sequence 18, Appli
15	2126	83.4	451	4	US-09-282-846-2	Sequence 2, Appli
16	2126	83.4	451	4	US-09-680-145-2	Sequence 2, Appli
17	2126	83.4	451	2	US-08-887-352B-14	Sequence 14, Appli
18	2124	83.3	451	2	US-08-887-352B-16	Sequence 16, Appli
19	2124	83.3	451	3	US-08-466-151-65	Sequence 65, Appli
20	2124	83.3	451	3	US-09-109-207C-14	Sequence 14, Appli
21	2124	83.3	451	3	US-09-109-207C-16	Sequence 16, Appli
22	2124	83.3	451	3	US-09-296-005-14	Sequence 14, Appli
23	2124	83.3	451	3	US-09-296-005-16	Sequence 16, Appli
24	2124	83.3	451	4	US-09-740-002-25	Sequence 25, Appli
25	2122.5	83.3	475	4	US-09-740-002-27	Sequence 27, Appli
26	2094.5	82.2	475	4	US-08-466-151-8	Sequence 8, Appli
27	2093	82.1	453	3		

28	2093	82.1	453	4	US-08-466-163B-8	Sequence 8, Appli
29	2072.5	81.3	462	4	US-09-289-942A-7	Sequence 7, Appli
30	2071.5	81.3	452	3	US-09-027-449-71	Sequence 71, Appli
31	2071.5	81.3	452	3	US-09-026-985-71	Sequence 71, Appli
32	2071.5	81.3	452	4	US-09-121-952A-71	Sequence 71, Appli
33	2071.5	81.3	452	4	US-09-234-340A-71	Sequence 71, Appli
34	2063	80.9	476	2	US-08-378-939-10	Sequence 10, Appli
35	2053.5	80.6	449	4	US-09-679-397-2	Sequence 2, Appli
36	2053.5	80.6	449	4	US-09-680-148-2	Sequence 2, Appli
37	2053.5	80.6	449	1	US-09-30-465A-2	Sequence 2, Appli
38	2053.5	80.6	459	7	US-09-157-101A-7	Sequence 7, Appli
39	2053	80.5	478	3	US-08-487-550-8	Sequence 8, Appli
40	2053	80.5	478	4	US-09-526-098-8	Sequence 8, Appli
41	2033	79.8	449	1	US-08-458-516-13	Sequence 13, Appli
42	2024.5	79.4	467	3	US-09-049-672A-8	Sequence 8, Appli
43	2016.5	79.1	454	2	US-07-934-373C-22	Sequence 22, Appli
44	2016.5	79.1	454	3	US-08-437-642B-22	Sequence 22, Appli
45	2016.5	79.1	454	4	US-08-146-206C-22	Sequence 22, Appli

```
                              ALIGNMENTS

RESULT 1
US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;  APPLICANT:  Anderson, Darrell R.
;  TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES:  12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;   STREET:  699 Prince Street
;   CITY:  Alexandria
;   STATE:  VA
;   COUNTRY:  USA
;   ZIP:  22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/487,550
;   FILING DATE:  07-JUN-1995
;   CLASSIFICATION:  435
;  ATTORNEY/AGENT INFORMATION:
;   NAME:  Teskin, Robin L.
;   REGISTRATION NUMBER:  35,030
;   REFERENCE/DOCKET NUMBER:  012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  703-836-6620
;   TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  12:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH:  476 amino acids
;    TYPE:  amino acid
;    TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-487-550-12

Query Match             100.0%;  Score 2549;  DB 3;  Length 476;
Best Local Similarity   100.0%;  Pred. No. 1.5e-198;
Matches  476;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
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;           MOLECULE TYPE: protein
US-09-526-098-12

Query Match           100.0%;  Score 2549;  DB 4;  Length 476;
Best Local Similarity 100.0%;  Pred. No. 1.5e-198;
Matches 476;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1  MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP  60

Qy     61  PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR  120

Qy    121  LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180

Qy    181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240

Qy    241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300

Qy    301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360
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Db    301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360

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RESULT 3
US-09-049-672A-4
;       Sequence 4, Application US/09049672A
;       Patent No. 6135941
;       GENERAL INFORMATION:
;         APPLICANT: Hillman, Jennifer L.
;         APPLICANT: Lal, Preeti
;         APPLICANT: Tang, Y. Tom
;         APPLICANT: Yue, Henry
;         APPLICANT: Au-Young, Janice
;         APPLICANT: Corley, Neil C.
;         APPLICANT: Guegler, Karl J.
;         APPLICANT: Baughn, Mariah R.
;         TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;         NUMBER OF SEQUENCES: 28
;         CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Incyte Pharmaceuticals, Inc.
;           STREET: 3174 Porter Drive
;           CITY: Palo Alto
;           STATE: CA
;           COUNTRY: USA
;           ZIP: 94304
;         COMPUTER READABLE FORM:
;           MEDIUM TYPE: Diskette
;           COMPUTER: IBM Compatible
;           OPERATING SYSTEM: DOS
;           SOFTWARE: FastSEQ for Windows Version 2.0
;         CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/049,672A
;           FILING DATE: HEREWITH
;           CLASSIFICATION: 536
;         PRIOR APPLICATION DATA:
;           APPLICATION NUMBER:
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Qy    121  LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
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Qy    181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
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Qy    241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300
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Db    241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300

Qy    301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360
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Qy    361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420
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Qy    421  KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
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RESULT 2
US-09-526-098-12
;       Sequence 12, Application US/09526098
;       Patent No. 6492134
;       GENERAL INFORMATION:
;         APPLICANT: Anderson, Darrell R.
;         TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;         TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;         TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;         TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;         NUMBER OF SEQUENCES: 12
;         CORRESPONDENCE ADDRESS:
;           ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;           STREET: 699 Prince Street
;           CITY: Alexandria
;           STATE: VA
;           COUNTRY: USA
;           ZIP: 22314
;         COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/526,098
;           FILING DATE:
;           CLASSIFICATION:
;         PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 09/383,916
;           FILING DATE:
;           APPLICATION NUMBER: US 08/487,550
;           FILING DATE: 07-JUN-1995
;         ATTORNEY/AGENT INFORMATION:
;           NAME: Teskin, Robin L.
;           REGISTRATION NUMBER: 35,030
;           REFERENCE/DOCKET NUMBER: 012712-131
;         TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 703-836-6620
;           TELEFAX: 703-836-2021
;       INFORMATION FOR SEQ ID NO: 12:
;         SEQUENCE CHARACTERISTICS:
;           LENGTH: 476 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:18:44 ; Search time 178.695 Seconds
                                            (without alignments)
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Perfect score: 2549
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                 Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158812981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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                18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2549	100.0	476	10	US-09-948-429B-12	Sequence 12, Appl
2	2549	100.0	476	12	US-10-124-807-12	Sequence 12, Appl
3	2549	100.0	476	12	US-10-291-532-12	Sequence 12, Appl
4	2549	100.0	476	14	US-10-124-905-12	Sequence 12, Appl
5	2309	90.6	476	10	US-09-948-429B-4	Sequence 4, Appli
6	2309	90.6	476	12	US-10-124-807-4	Sequence 4, Appli
7	2309	90.6	476	12	US-10-291-532-4	Sequence 4, Appli
8	2309	90.6	476	14	US-10-124-905-4	Sequence 4, Appli
9	2145.5	84.2	467	15	US-10-211-357-12	Sequence 12, Appl
10	2144.5	84.1	467	15	US-10-211-357-8	Sequence 8, Appli
11	2138	83.9	580	12	US-10-310-719-37	Sequence 37, Appl
12	2137.5	83.9	467	15	US-10-211-357-10	Sequence 10, Appl
13	2127	83.4	451	11	US-09-925-179-66	Sequence 66, Appl
14	2126	83.4	451	9	US-09-920-171-18	Sequence 18, Appl
15	2126	83.4	451	12	US-10-113-996-18	Sequence 18, Appl
16	2126	83.4	451	12	US-10-292-869-2	Sequence 2, Appli
17	2126	83.4	451	12	US-09-792-938-2	Sequence 2, Appli
18	2124	83.3	451	9	US-09-920-171-14	Sequence 14, Appl
19	2124	83.3	451	9	US-09-920-171-16	Sequence 16, Appl
20	2124	83.3	451	11	US-09-925-179-65	Sequence 65, Appl
21	2124	83.3	451	12	US-10-113-996-14	Sequence 14, Appl
22	2124	83.3	451	12	US-10-113-996-16	Sequence 16, Appl
23	2122.5	83.3	450	10	US-09-796-848A-43	Sequence 43, Appl
24	2122.5	83.3	450	10	US-09-996-288-218	Sequence 218, App
25	2122.5	83.3	450	10	US-09-996-288-250	Sequence 250, App
26	2122.5	83.3	450	11	US-09-996-265-218	Sequence 218, App
27	2122.5	83.3	450	11	US-09-996-265-250	Sequence 250, App
28	2122.5	83.3	475	9	US-09-740-002-25	Sequence 25, Appl
29	2121	83.2	451	11	US-09-925-179-68	Sequence 68, Appl
30	2120.5	83.2	450	9	US-09-796-848A-49	Sequence 49, Appl
31	2120.5	83.2	450	10	US-09-996-288-216	Sequence 216, App
32	2120.5	83.2	450	11	US-09-996-265-216	Sequence 216, App
33	2119.5	83.2	450	9	US-09-796-848A-39	Sequence 39, Appl
34	2119.5	83.2	450	9	US-09-796-848A-41	Sequence 41, Appl
35	2119.5	83.2	450	10	US-09-996-288-222	Sequence 222, App
36	2119.5	83.2	450	10	US-09-996-288-224	Sequence 224, App
37	2119.5	83.2	450	11	US-09-996-265-222	Sequence 222, App
38	2119.5	83.2	450	11	US-09-996-265-224	Sequence 224, App
39	2118.5	83.1	450	9	US-09-796-848A-37	Sequence 37, Appl
40	2118.5	83.1	450	10	US-09-996-288-220	Sequence 220, App
41	2118.5	83.1	450	11	US-09-996-265-220	Sequence 220, App
42	2117.5	83.1	450	9	US-09-796-848A-45	Sequence 45, Appl
43	2117.5	83.1	450	10	US-09-996-288-226	Sequence 226, App
44	2117.5	83.1	450	10	US-09-996-288-252	Sequence 252, App
45	2117.5	83.1	450	10	US-09-996-288-254	Sequence 254, App

ALIGNMENTS

RESULT 1
US-09-948-429B-12
; Sequence 12, Application US/09948429B
Patent No. US20020177689A1
; GENERAL INFORMATION:
     APPLICANT: Anderson, Darrell R.
     TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
     TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
     TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
     TITLE OF INVENTION: IMMUNOSUPPRESANTS"
     NUMBER OF SEQUENCES: 12
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
          STREET: 699 Prince Street
          CITY: Alexandria
          STATE: VA
          COUNTRY: USA
          ZIP: 22314
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/948,429B
          FILING DATE:
          CLASSIFICATION:
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 09/383,916
          FILING DATE:
          APPLICATION NUMBER: US 08/487,550
          FILING DATE: 07-JUN-1995
     ATTORNEY/AGENT INFORMATION:
          NAME: Teskin, Robin L.
          REGISTRATION NUMBER: 35,030
          REFERENCE/DOCKET NUMBER: 012712-131
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: 703-836-6620

;   TELEFAX: 703-836-2021
;   INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 476 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-948-429B-12

Query Match   100.0%; Score 2549; DB 10; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-172;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
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Db   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDR 120

Qy   121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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Db   121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

Qy   181 EPVTVSNNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
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Db   181 EPVTVSNNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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Qy   301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
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Qy   361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
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Db   361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Qy   421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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Db   421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476

RESULT 2
US-10-124-807-12
; Sequence 12, Application US/10124807
; Publication No. US20030156207A1
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/124,807
;   FILING DATE:
;   CLASSIFICATION:

;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 476 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-10-124-807-12

Query Match   100.0%; Score 2549; DB 12; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-172;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
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Qy   121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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Qy   181 EPVTVSNNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
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Db   181 EPVTVSNNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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Qy   301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
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RESULT 3
US-10-291-532-12
; Sequence 12, Application US/10291532
; Publication No. US2003018029OA1
; GENERAL INFORMATION:
;   APPLICANT: HARIHARAN, KANDASAMY
;   APPLICANT: HANNA, NABIL
;   TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
;   TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
;   TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
;   FILE REFERENCE: 037003/291872
;   CURRENT APPLICATION NUMBER: US/10/291,532
;   CURRENT FILING DATE: 2002-11-12
;   PRIOR APPLICATION NUMBER: 60/331,187
;   PRIOR FILING DATE: 2001-11-09
;   PRIOR APPLICATION NUMBER: 09/758,173

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/526,098
  FILING DATE:
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/383,916
  FILING DATE:
  APPLICATION NUMBER: US 08/487,550
  FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
  NAME: Teskin, Robin L.
  REGISTRATION NUMBER: 35,030
  REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 703-836-6620
  TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 705 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: not relevant
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
  FEATURE:
  NAME/KEY: CDS
  LOCATION: 1..705
  FEATURE:
  NAME/KEY: mat_peptide
  LOCATION: 1..705
US-09-526-098-1

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Query Match             100.0%;  Score 705;  DB 4;  Length 705;
Best Local Similarity   100.0%;  Pred. No. 3.7e-186;
Matches  705;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 ATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTGCTCGTCTGGGCTCCCAGGTGCACGATGT 60
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Qy   61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATC 120
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Qy  121 ACCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGTACCAGCAGAAGCCAGCG 180
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Qy  301 GATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGA 360
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Qy  361 GGAGGGACCCGGGTGACCGTGCCCCTGCCCCTCGGTCACTCTGTTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GGAGGGACCCGGGTGACCGTGCCCCTGCCCCTCGGTCACTCTGTTC 420

Qy  421 CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  481 TTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGA 540
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Qy  541 GTGGAGACCACCACACCCTCCAAACAAGCAACAACAAAGCAACAACAGTACGGGCCAGCTACCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GTGGAGACCACCACACCCTCCAAACAAGCAACAACAAAGCAACAACAGTACGGGCCAGCTACCTG 600

Qy  601 AGCCTGACGCCTGAGCAGTGGAAGTCCACAGAAGTCACAGAAGCTGCCAGGTCACGCATGAA 660
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Qy  661 GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
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Db  661 GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
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RESULT 2
US-09-526-098-1
; Sequence 1, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
    APPLICANT: Anderson, Darrell R.
    TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
    TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
    TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
    TITLE OF INVENTION: IMMUNOSUPPRESANTS"
    NUMBER OF SEQUENCES: 12
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
    STREET: 699 Prince Street
    CITY: Alexandria
    STATE: VA
    COUNTRY: USA
    ZIP: 22314
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible

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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October  2, 2003, 13:10:05 ; Search time 37.4685 Seconds
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Title:          US-09-758-173-1
Perfect score:  705
Sequence:       1 ATGAGGGTCCCGCTCAGCT........CCCCTACAGAATGTTCATGA 705

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       56978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:     1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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	2	705	100.0	705	4	US-09-526-098-1	Sequence 1, Appli
	3	585.2	83.0	702	3	US-08-523-894-5	Sequence 5, Appli
	4	540.2	76.6	711	4	US-08-487-550-9	Sequence 9, Appli
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	7	457	64.8	902	3	US-08-378-939-11	Sequence 11, Appl
	8	456	64.7	895	3	US-09-049-672A-25	Sequence 25, Appl
	9	455.4	64.6	891	3	US-09-049-672A-23	Sequence 23, Appl
	10	440	62.4	705	4	US-09-372-425A-3	Sequence 3, Appli
	11	435.6	61.8	885	4	US-09-152-060-47	Sequence 47, Appl
	12	434	61.6	879	4	US-09-152-060-29	Sequence 29, Appli
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	14	425.4	60.3	919	3	US-09-049-672A-24	Sequence 24, Appl
	15	407.4	57.8	716	4	US-08-793-450-5	Sequence 5, Appli
c	16	392.4	55.7	491	4	US-09-702-705-833	Sequence 833, App
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	18	388.2	55.1	805	4	US-09-620-312D-62	Sequence 62, Appl
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ALIGNMENTS

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US-08-487-550-1

; Sequence 1, Application US/0848755O
; Patent No. 6113898
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/487,550
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 705 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: not relevant
;    TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;    NAME/KEY: CDS
;    LOCATION: 1..705
;   FEATURE:
;    NAME/KEY: mat_peptide
;    LOCATION: 1..705
US-08-487-550-1

Query Match             100.0%;  Score 705;  DB 3;  Length 705;
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VERSION     BQ709526.1  GI:21848425
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 931)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2474  row: 1  column: 21
            High quality sequence stop: 653.
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                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT     227 a    284 c    245 g    174 t    1 others
ORIGIN

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Best Local Similarity   89.3%;  Pred. No. 1.7e-125;
Matches   623;   Conservative    0;   Mismatches   69;   Indels    6;   Gaps    2;

Qy     11 CGGCTCAGCTCCTGGGGCTTCCTCGTCTCCTGGCTTCCCAGGTGCACGATCGCCTATGAAC  70
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Db     37 CCGTTCTCCCTCGGCCTCCTCTCTCACTG---CACAGGCTCTGTGACCTCCTATGTGC  93

Qy     71 TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGGCTCACCTGTGGGG  130
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Db     94 TGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGGCCAACATTACCTGTGTGG  153

Qy    131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGAGCCAGGCGCGGGCCCTA  190
             ||| ||| || ||||| |||| ||||||||||||||| ||||| | |||||||||
Db    154 GAAACAATATTGGAAGTAAAAGTGTGCACTGGTACCACGAGAGGCCAGCAGCCCCTG  213

Qy    191 TACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTGGCT  250
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Db    214 TGCTGGTCGTCAATGATGACAGCAGCGGCGGCCCCTCAGGGATCCCTGAGCGATTCTGGCT  273

Qy    251 CCAAATCAGGGAACACCGCACCGCACCCTGACCATCAACGGGGTCGGGGATGAGGCTG  310
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Db    274 CCAACTCTGGAAACACCACGGCACCCTGACCATCGACCAGGGTCGAAGCGGGGATGAGGCCG  333

Qy    311 ACTATTACTGTCAGTGTGGGACAGGCTAGTGATCATC---CGGTCTTCGGAGGAGGGA  367
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Qy    368 CCCGGGTGACCGTCCTAGGTCAGCCAAGGCTCAGCCCCGTCACTCTGTTCCCGCCCT  427
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Query Match             79.3%;  Score 558.8;  DB 13;  Length 952;
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Db     23 CCTATGTGCCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAGAGACGGCCAGGATTA  82

Qy    122 CCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC  181
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Db     83 CCTGTGAGGGAAAACAACAATTGGAGGTAAAAGTGTGCACTGGTACCAGCAGAAGGCCAGGCC  142

Qy    182 GGGCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGATCCCTGAGCGAT  241
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Qy    242 TCTCTGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGTCGAGGCCGGG  301
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                Copyright   GenCore version 5.1.6
                Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       October  2, 2003, 13:05:20 ; Search time 1165.91 Seconds
                                           (without alignments)
                                           14696.420 Million cell updates/sec

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Perfect score: 705
Sequence:     1 ATGAGGGTCCCCGCTCAGCT........CCCCTACAGAATGTTCATGA 705

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:   45562784

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
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6	551.2	78.2	921	13	BQ708246	BQ708246 AGENCOURT
7	548.8	77.6	920	13	BQ712280	BQ712280 AGENCOURT
8	547.2	77.4	925	10	BQ710672	BQ710672 AGENCOURT
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31	520.8	73.9	913	10	BG745387	BG745387 602723726
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38	512.6	72.7	864	10	BG756128	BG756128 602713428
39	512.6	72.3	958	13	BU146944	BU146944 AGENCOURT
40	510	72.1	782	12	BM007795	BM007795 603617259
41	508.4	72.1	801	12	BM007626	BM007626 603617044
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44	501.8	71.2	688	10	BG745481	BG745481 602724051
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ALIGNMENTS

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BQ711447
LOCUS       BQ711447       952 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353624 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279618
            5', mRNA sequence.
ACCESSION   BQ711447
VERSION     BQ711447.1  GI:21850346
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 952)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469 row: h  column: 19
            High quality sequence stop: 584.
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```
XX
DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01817.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 7; Fig 8A; 81pp; English.
XX
CC   2 DNA sequences (AAT62509 and AAT62510) respectively code for
CC   primatised forms (AAW01817 and AAW01818) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   7C10.  Cloned 7C10 light and heavy variable genes are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells.  Primatised 7B6 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01819-22).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match             100.0%;  Score 705;  DB 18;  Length 705;
Best Local Similarity   100.0%;  Pred. No. 4.3e-167;
Matches   705;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy    121 ACCTGTGGGGGAGACACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180
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Db    181 CGGGCCCCTATACTGGTCATCTATGATGATGATAGTGACCGGCCCTGAGGGATCCCTGAGCGA 240

Qy    241 TTCTCTGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGTCGAGGCCGGG 300
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Qy    301 GATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGA 360
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Db    301 GATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGA 360

Qy    361 GGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCACTCGTTC 420
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Db    361 GGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCACTCGTTC 420

Qy    421 CCGCCCTTCCTGAGGAGCTTCAAGCAACAAGGCCACACTGTGTCTCATAAGTGAC 480
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Db    421 CCGCCCTTCCTGAGGAGCTTCAAGCAACAAGGCCACACTGTGTCTCATAAGTGAC 480

Qy    481 TTCTACCCGGAGCCCGTGACAGTGGCCTGAAGGCAGATAGCAGCCCCGTCAAGGCGGGA 540
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Qy    541 GTGGAGACCACCACACCCTCCAAACAACAACAACAAGTACGCGGCCAGCAGCTACCTG 600
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Qy    601 AGCCTGACGCGCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTCACGCATGAA 660
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Qy    661 GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
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Db    661 GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705

RESULT 2
AAV35484
ID   AAV35484 standard; DNA; 705 BP.
XX
AC   AAV35484;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 7C10 light chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..705
FT                   /*tag= a
FT                   /product= 7C10 light chain
XX
PN   WO981970-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US19906.
PR   08-NOV-1996;   96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63760.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 3a; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 7C10 light chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match             100.0%;  Score 705;  DB 19;  Length 705;
Best Local Similarity   100.0%;  Pred. No. 4.3e-167;
Matches   705;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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                GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   October  2, 2003, 12:12:30  ; Search time 144.396 Seconds
                                         (without alignments)
                                       13179.730 Million cell updates/sec

Title:          US-09-758-173-1
Perfect score:  705
Sequence:     1 ATGAGGGTCCCCGCTCAGCT........CCCCTACAGAATGTTCATGA 705

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2552756 seqs, 134919017 residues

Total number of hits satisfying chosen parameters:        5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	705	100.0	705	18	AAT62509	Primatised anti-hu
2	705	100.0	705	19	AAV35484	Macaque primatized
3	705	100.0	705	24	AAS17242	DNA sequence of a
4	585.2	83.0	702	18	AAT62867	Ant-CD4 monkey-hum
5	582.6	82.6	926	20	AA224427	Human bladder tumo
6	558.6	79.2	699	25	ABX12862	DNA encoding monoc
7	555.6	78.8	836	23	AAS83482	DNA encoding novel
8	540.2	76.6	711	19	AAV35488	Macaque primatized

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 9  540.2  76.6   711  24  AAS17246   DNA sequence of a
10  538.6  76.4   711  18  AAT62512   Primatised anti-hu
11  527.6  74.8  1027  24  ABQ54438   Human ovarian anti
12    524   74.3   841  23  AAS83486   DNA encoding novel
13  520.8  73.9   904  24  ABK28671   Human cDNA encodin
14  520.4  73.8   869  22  AAS22217   Human cDNA encodin
15    518  73.5   702  24  ABS67760   DNA encoding antib
16    518  73.2   702  24  ABS63406   DNA encoding human
17  516.4  73.2   830  25  ABT31878   Anti-CD40 monoclon
18    516  73.2   791  23  AAS87271   DNA encoding novel
19    515  73.0  1825  22  AAS22777   Human cDNA encodin
20  514.4  73.0   859  22  AAS22481   Human cDNA encodin
21  512.8  72.7   960  21  AAC78188   Human cancer assoc
22    512  72.6   872   9  AAN81655   VDJC regions of hu
23    511  72.5   654  22  AAS13364   Human cDNA encodin
24  509.2  72.2   930  22  AAS22541   Human cDNA encodin
25    506  71.8   793  23  AAS83481   DNA encoding novel
26    504  71.5   807  23  AAS83484   Human cDNA encodin
27  495.2  70.2   863  24  ABK28650   Human cDNA encodin
28    490  69.5   886  22  ABQ93531   Human cDNA SEQ ID
29    480  68.1   849  22  AAH98186   Human EST-derived
30  475.8  67.5   870  24  AAL50812   Human cancer statu
31  474.2  67.3   884  11  AAQ03509   Sequence encoding
32  473.6  67.2   810  23  AAS87270   DNA encoding novel
33    473  67.1   935  22  AAC66525   Human immune syste
34    472  67.0   768  20  AAX06953   Monoclonal antibod
35    472  67.0   768  20  AAX06954   Monoclonal antibod
36  465.6  66.0   826  22  AAI58109   Human polynucleoti
37  462.8  65.6   915  24  ABN97248   Gene #3746 used to
38  462.8  65.6   915  24  ABK64815   Human benign prost
39  462.8  65.6   915  24  ABL5478    Lung cancer relate
40  462.8  65.6   964  24  ABQ93374   Human cDNA SEQ ID
41  462.2  65.6   654  14  AAQ49835   Anti-HIV-1 recombi
42    462  65.5   762  22  AAC84209   Plasmid Glambda-1B
43    462  65.5  5679  22  AAC84207   Plasmid Glambda-1A
44  461.8  65.5   889  23  AAS77073   DNA encoding novel
45    457  64.8   902  14  AAQ35100   Antibody D lambda
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ALIGNMENTS

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RESULT 1
AAT62509
ID   AAT62509 standard; DNA; 705 BP.
XX
AC   AAT62509;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7C10 light chain DNA.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
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PN   WO9640878-A1.
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PD   19-DEC-1996.
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PF   06-JUN-1996;  96WO-US10053.
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PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
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PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
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FEATURES
source

Location/Qualifiers
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/organism="unknown"

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ORIGIN

Query Match   100.0%; Score 705; DB 6; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  601 AGCCTGACGCTGAGCAGTGGAAGTCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA 660
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FEATURES
source

Location/Qualifiers
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/organism="unknown"

BASE COUNT   162 a   214 c   207 g   122 t
ORIGIN

Query Match   100.0%; Score 705; DB 6; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  421 CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC 480
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Qy  481 TTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAGGCGGGA 540
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Db  481 TTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAGGCGGGA 540

Qy  541 GTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTACCTG 600
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Db  541 GTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTACCTG 600

Qy  601 AGCCTGACGCTGAGCAGTGGAAGTCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA 660
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Db  601 AGCCTGACGCTGAGCAGTGGAAGTCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA 660

Qy  661 GGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCATGA 705
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RESULT 2
AR265196
LOCUS   AR265196   705 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6492134.
ACCESSION   AR265196
VERSION   AR265196.1 GI:29693617
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 705)
  AUTHORS   Aquin,S. and Vezina,Louis.-P.
  TITLE   Method for producing polyhydroxyalkanoates in recombinant organisms
  JOURNAL   Patent: US 6492134-A 1 10-DEC-2002;

RESULT 3
BD063034
LOCUS   BD063034   705 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION Identification of unique binding interactions between certain
            antibodies and the human B7.1 and B7.2 co-stimulatory antigens.
ACCESSION   BD063034
VERSION   BD063034.1 GI:22608637
KEYWORDS   JP 2001504693-A/1.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 705)
  AUTHORS   Anderson,D.R., Hanna,N., Brams,P. and Hard,C.

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: October 2, 2003, 13:01:50 ; Search time 1851.84 Seconds
(without alignments)
15574.362 Million cell updates/sec

Title: US-09-758-173-1
Perfect score: 705
Sequence: 1 ATGAGGGTCCCCGCTCAGCT.........CCCCTACAGAATGTTCATGA 705

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   GenEmbl:*
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2: gb_htg:*
3: gb_in:*
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32: em_htg_other:*
33: em_htg_mus:*
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35: em_htg_rod:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	705	100.0	705	6	AR265196	AR265196 Sequence
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4	585.2	83.0	702	6	AR135374	AR135374 Sequence
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6	571.2	81.0	901	9	BC028090	BC028090 Homo sapi
7	569.8	80.8	803	9	HSIGVL022	X57812 Human rearr
8	561.8	79.7	747	9	HSIGVL031	X57821 Human rearr
9	558.6	79.2	699	9	AY172962	AY172962 Homo sapi
10	542.8	77.0	648	9	HSA309319	AJ309319 Homo sapi
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13	540.2	76.6	711	6	BD063038	BD063038 Identific
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15	534.4	75.8	826	9	AB064174	AB064174 Homo sapi
16	529.6	75.1	824	9	AB064176	AB064176 Homo sapi
17	526.4	74.7	813	9	AB064167	AB064167 Homo sapi
18	525.2	74.5	895	9	BC022823	BC022823 Homo sapi
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21	522	74.0	788	9	AB064168	AB064168 Homo sapi
22	520.8	73.9	904	6	AX402510	AX402510 Sequence
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25	516.4	73.2	830	6	BD182349	BD182349 Anti CD40
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27	514.4	73.0	839	9	HSIGVL026	X57816 Human rearr
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40	504	71.5	806	9	HSIGVL005	X57805 Human rearr
41	501.8	71.2	647	9	AB087878	AB087878 Homo sapi
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ALIGNMENTS

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LOCUS   AR108862   705 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION   Sequence 1 from patent US 6113898.
ACCESSION   AR108862
VERSION   AR108862.1 GI:12825138
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 705)
AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE   Human B7.1-specific primatized antibodies and transfectomas
             expressing said antibodies
JOURNAL   Patent: US 6113898-A 1 05-SEP-2000;

Pred. No. is the number of results predicted by chance to have a

GenCore version 5.1.6
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Run on: October 2, 2003, 19:53:01 ; Search time 139.466 seconds
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12894.584 Million cell updates/sec

Title: US-09-758-173-1
Perfect score: 705
Sequence: 1 ATGAGGGTCCCGCGCTCAGCT........CCCCTACAGAATGTTCATGA 705

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	705	100.0	705	10	US-09-948-429B-1	Sequence 1, Appli
2	705	100.0	705	12	US-10-124-807-1	Sequence 1, Appli
3	705	100.0	705	12	US-10-291-532-1	Sequence 1, Appli
4	705	100.0	705	13	US-10-124-905-1	Sequence 1, Appli
5	705	100.0	705	13	US-10-073-138-1	Sequence 1, Appli
6	585.2	83.0	702	14	US-10-211-357-5	Sequence 5, Appli
7	558.6	79.2	699	12	US-10-225-108A-11	Sequence 11, Appl
8	555	78.7	1402	14	US-10-198-846-12610	Sequence 12610, A
9	552.6	78.4	642	11	US-09-972-656-95	Sequence 95, Appl
10	540.2	76.6	711	10	US-09-948-429B-9	Sequence 9, Appli
11	540.2	76.6	711	12	US-10-124-807-9	Sequence 9, Appli
12	540.2	76.6	711	12	US-10-291-532-9	Sequence 9, Appli
13	540.2	76.6	711	13	US-10-124-905-9	Sequence 9, Appli
14	540.2	76.6	711	13	US-10-073-138-5	Sequence 5, Appli
15	539.6	76.5	1590	14	US-10-198-846-12799	Sequence 12799, A
16	530	75.2	868	9	US-09-822-849A-157	Sequence 157, App
17	520.8	73.9	1123	14	US-10-198-846-13547	Sequence 13547, A
18	516	73.2	859	14	US-10-198-846-13995	Sequence 13995, A
19	512.8	72.7	960	9	US-09-925-301-582	Sequence 582, App
20	511	72.5	654	11	US-09-791-153A-50	Sequence 50, Appl
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22	505.6	71.7	895	14	US-10-198-846-12838	Sequence 12838, A
23	501.6	71.1	830	10	US-09-981-353-42	Sequence 42, Appl
24	494	70.1	849	14	US-10-198-846-12585	Sequence 12585, A
25	492.6	69.9	636	11	US-09-972-656-97	Sequence 97, Appl
26	488.6	69.3	846	10	US-09-981-353-55	Sequence 55, Appl
27	487	69.1	1480	10	US-09-981-353-146	Sequence 146, App
28	473.8	67.2	857	9	US-09-822-849A-158	Sequence 158, App
29	472	67.0	768	10	US-09-747-669-4	Sequence 4, Appli
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31	472	67.0	768	14	US-10-290-703-4	Sequence 4, Appli
32	472	67.0	768	14	US-10-290-703-5	Sequence 5, Appli
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34	469.4	66.6	1640	14	US-10-198-846-13206	Sequence 13206, A
35	465.6	66.0	826	13	US-10-098-841-316	Sequence 316, App
36	465	66.0	1640	14	US-10-198-846-13206	Sequence 13206, A
37	463.2	65.7	848	14	US-10-158-646-70	Sequence 70, Appl
38	463	65.7	888	14	US-10-158-646-71	Sequence 71, Appl
39	462.8	65.6	915	10	US-09-954-456-788	Sequence 788, App
40	462.8	65.6	915	10	US-09-880-107-3743	Sequence 3743, Ap
41	462.8	65.6	915	12	US-09-873-319-710	Sequence 710, App
42	462.8	65.6	915	12	US-09-960-706-1069	Sequence 1069, Ap
43	461.8	65.5	883	14	US-10-158-646-73	Sequence 73, Appl
44	457.2	64.9	670	11	US-09-968-433-40	Sequence 40, Appl
45	456	64.7	2635	14	US-10-198-846-13529	Sequence 13529, A

ALIGNMENTS

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RESULT 1
US-09-948-429B-1
; Sequence 1, Application US/0994429B
; Patent No. US20020017689A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/948,429B
;   FILING DATE:
;   CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
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;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;       STREET: 699 Prince Street
;       CITY: Alexandria
;       STATE: VA
;       COUNTRY: USA
;       ZIP: 22314
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/124,807
;       FILING DATE:
;       CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 09/383,916
;       FILING DATE:
;       APPLICATION NUMBER: US 08/487,550
;       FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Teskin, Robin L.
;       REGISTRATION NUMBER: 35,030
;       REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 703-836-6620
;       TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 705 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: not relevant
;       TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 1..705
;   FEATURE:
;       NAME/KEY: mat_peptide
;       LOCATION: 1..705
US-10-124-807-1

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;       LENGTH: 705 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: not relevant
;       TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 1..705
;   FEATURE:
;       NAME/KEY: mat_peptide
;       LOCATION: 1..705
US-09-948-429B-1

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Matches  705;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy     61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATC 120
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Qy    121 ACCTGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180
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Db    121 ACCTGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180

Qy    181 CGGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGA 240

Qy    241 TTCTCTGGCTCCAAATCAGGGAACACCGCACCCTGACCAACGGGGTCGAGGCCGGG 300
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Qy    301 GATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGCTAGTGATCATCCGGTCTTCGGA 360
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Db    481 TTCTACCCGGGAGCCGGCCGTGACAGTGGCCTGGAAGGCAGAGCCAGTCAAGGCGGGA 540

Qy    541 GTGGAGACCACCACCCTCCAAACAAACAACAAGCAACAACAAGTACGCGGCCAGCTACCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGGAGACCACCACCCTCCAAACAAACAACAAGCAACAACAAGTACGCGGCCAGCTACCTG 600

Qy    601 AGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGTGCCAGGTTCACCGATGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGTGCCAGGTTCACCGATGAA 660

Qy    661 GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
          |||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705

RESULT 2
US-10-124-807-1
; Sequence 1, Application US/10124807
; Publication No. US20030162207A1
; GENERAL INFORMATION:
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 27.4586 Seconds
                                               (without alignments)
                                               1352.654 Million cell updates/sec

Title: US-09-758-173-2
Perfect score: 1243
Sequence: 1 MRVPAQLLGLLLLWLPGARC........CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 15872657 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_19Jun03:*
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           13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
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           24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1243	100.0	234	18	AAW01817	Primatised anti-hu
2	1243	100.0	234	19	AAW63760	Macaque primatized
3	1243	100.0	234	23	AAU11538	Protein sequence o
4	1015.5	81.7	233	18	AAW14924	Ant-CD4 monkey-hum
5	1001	80.5	232	24	ABU08020	Monoclonal rabies
6	991.5	79.8	247	22	ABG19295	Novel human diagno
7	979	78.8	238	22	ABG19299	Novel human diagno
8	976.5	78.6	232	22	AAU14412	Human novel protei
9	973	78.3	236	19	AAW63764	Macaque primatized

10	973	78.3	236	23	AAU11645	Protein sequence o
11	973	78.0	269	23	ABP41361	Human ovarian anti
12	970	78.0	236	18	AAW01821	Primatised anti-hu
13	967.5	77.8	212	24	ABR01497	Human anti-TIMP-1
14	966	77.7	212	24	ABR01474	Human anti-TIMP-1
15	960.5	77.3	212	24	ABR01489	Human anti-TIMP-1
16	959	77.2	231	22	AAU14176	Human novel protei
17	959	77.2	234	22	ABG23084	Novel human diagno
18	958.5	77.1	232	22	AAU14236	Human novel protei
19	958	77.1	211	24	ABR01495	Human anti-TIMP-1
20	956.5	77.0	212	24	ABR01486	Human anti-TIMP-1
21	955	76.8	235	23	ABP63052	Human polypeptide
22	953	76.7	211	24	ABR01472	Human anti-TIMP-1
23	951	76.5	211	24	ABR01471	Human anti-TIMP-1
24	946	76.1	231	24	ABJ36936	Anti-CD40 monoclon
25	944	75.9	218	22	AAU08381	Anti-OPGbp antibod
26	944	75.9	233	23	AAU82012	Human secreted pro
27	939.5	75.6	236	22	AAU14472	Human novel protei
28	936.5	75.3	244	21	AAB43979	Human cancer assoc
29	936	75.3	226	22	ABG19294	Novel human diagno
30	934	75.1	233	23	ABG91843	Human antibody fra
31	934	75.1	233	23	ABG78152	Human Fv molecule
32	925	74.4	233	9	AAP81260	VDJC regions of hu
33	915	73.6	233	23	ABG92022	Antibody protein #
34	912	73.4	231	23	AAU81991	Human secreted pro
35	906.5	72.9	232	22	AAM23527	Human EST encoded
36	905	72.8	238	22	ABG19297	Novel human diagno
37	898.5	72.3	246	22	ABB12413	Human bone marrow
38	890.5	71.6	216	24	ABR01473	Human anti-TIMP-1
39	890	71.6	242	24	ABU08021	Monoclonal rabies
40	886	71.2	234	24	ABG73422	Human IgG anti-rhe
41	885.5	71.2	215	24	ABR01482	Human anti-TIMP-1
42	885	71.2	215	24	ABR01493	Human anti-TIMP-1
43	885	71.2	215	24	ABR01496	Human anti-TIMP-1
44	884.5	71.2	217	14	AAR42163	Anti-HIV-1 recombi
45	881	70.9	236	22	ABG23083	Novel human diagno

ALIGNMENTS

RESULT 1
AAW01817
ID   AAW01817 standard; Protein; 234 AA.
XX
AC   AAW01817;
XX
DT   25-MAY-1997 (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7C10 light chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996; 96WO-US10053.
XX
PR   07-JUN-1995; 95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX

```
DR   WPI; 1997-108638/10.
DR   N-PSDB; AAT62509.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 6; Fig 8A; 81pp; English.
XX
CC   2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy
CC   variable genes (see also AAT62509 and AAT62510) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01819-22). The
CC   primatised antibodies inhibit the B7;CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence   234 AA;

Query Match      100.0%;    Score 1243;   DB 18;   Length 234;
Best Local Similarity  100.0%;    Pred. No. 1e-70;
Matches  234;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MRVPAQLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRVPAQLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60

Qy   61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120

Qy  121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

Qy  181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 2
AAW63760
ID   AAW63760 standard; Protein; 234 AA.
XX
AC   AAW63760;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 7C10 light chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; interaction; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US19906.
XX
PR   08-NOV-1996;   96US-0746351.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
```

```
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35484.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 3a; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 7C10 light
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. Mab's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence   234 AA;

Query Match      100.0%;    Score 1243;   DB 19;   Length 234;
Best Local Similarity  100.0%;    Pred. No. 1e-70;
Matches  234;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MRVPAQLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRVPAQLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60

Qy   61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120

Qy  121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

Qy  181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 3
AAU11538
ID   AAU11538 standard; Protein; 234 AA.
XX
AC   AAU11538;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Protein sequence of primatised form of the light chain of 7C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; mutein.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
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                    GenCore version 5.1.6
         Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  2, 2003, 09:07:34  ; Search time 10.2833 Seconds
                                         (without alignments)
                                         2188.349 Million cell updates/sec

Title:     US-09-758-173-2
Perfect score:  1243
Sequence:  1 MRVPAQLLGLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 234

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:  283308 seqs, 96168582 residues

Total number of hits satisfying chosen parameters:    283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    PIR_76:*
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          2:  pir2:*
          3:  pir3:*
          4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1016	81.7	232	2	S25756	Ig lambda chain -
2	1012.5	81.5	233	2	S25747	Ig lambda chain -
3	979	78.8	231	2	S25738	Ig lambda chain -
4	959	77.2	231	2	S25751	Ig lambda chain -
5	959	77.2	231	2	S25753	Ig lambda chain -
6	936	75.3	226	2	S25745	Ig lambda chain -
7	923	74.3	213	2	JE0247	Ig lambda chain NI
8	920	74.0	233	2	S25748	Ig lambda chain -
9	920	74.0	235	2	S05270	Ig lambda chain pr
10	910	73.2	232	2	S25742	Ig lambda chain -
11	905	72.8	233	2	S25741	Ig lambda chain -
12	883	71.0	233	2	S25752	Ig lambda chain v
13	881	70.9	235	2	S25750	Ig lambda chain -
14	873	70.2	234	2	S25757	Ig lambda chain -
15	871.5	70.1	213	2	S21066	Ig lambda chain -
16	871.5	70.1	236	2	S25746	Ig lambda chain v
17	870	70.0	233	2	S25744	Ig lambda chain -
18	870	70.0	235	2	S14675	Ig lambda chain -
19	867.5	69.8	235	2	S25759	Ig lambda chain -
20	867	69.8	216	2	A42193	Ig lambda chain (B
21	862.5	69.4	217	2	JE0246	Ig lambda chain NI
22	859	69.1	216	2	S29258	Ig lambda chain v
23	850.5	68.4	235	2	S25754	Ig lambda chain -
24	846	68.1	216	2	S03401	Ig lambda chain (K
25	840.5	67.6	235	2	S25758	Ig lambda chain -
26	835	67.2	190	2	S25740	Ig lambda chain -
27	833.5	67.1	212	2	S70431	Ig lambda chain -
28	822	66.1	216	2	JE0245	Ig lambda chain NI
29	820.5	66.0	235	2	S25749	Ig lambda chain -
30	818	65.8	216	2	S69130	Ig lambda chain (D
31	799	64.3	208	2	B49444	Ig lambda chain (N
32	785	63.2	243	2	S25755	Ig lambda chain -
33	639.5	51.4	181	2	PT0220	Ig lambda chain V-
34	639.5	51.4	232	2	S17399	Ig lambda chain pr
35	635.5	51.1	214	2	PC4156	Ig lambda chain V
36	632	50.8	230	2	S49449	Ig lambda chain -
37	622.5	50.1	213	2	A21177	Ig light chain pre
38	603	48.5	118	2	S12441	Ig lambda chain (K
39	600	48.3	118	2	S12442	Ig lambda chain (K
40	579	46.6	118	2	S12440	Ig lambda chain (M
41	578	46.5	118	2	S12443	Ig lambda chain (K
42	576	46.3	118	2	A39949	Ig lambda chain J-
43	559	45.0	234	2	A39956	Ig lambda chain pr
44	548	44.1	105	1	L2HU	Ig lambda chain C
45	542.5	43.6	146	2	S02083	Ig lambda chain V-

ALIGNMENTS

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RESULT 1
S25756
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25756
R;Combriato, G.; Klobeck, H.G.
  Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25756
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-232 <COM>
A;Cross-references: EMBL:X57821; NID:g33741; PIDN:CAA40958.1; PID:g33742
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

Query Match         81.7%;  Score 1016;  DB 2;  Length 232;
Best Local Similarity 86.0%;  Pred. No. 8.7e-61;
Matches  196;  Conservative  14;  Mismatches  16;  Indels  2;  Gaps  2;

Qy      7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV 66
            ||||:||||||||::|:|!|||||:||:|!|:|||||||:||:::!:|!||:||||||||
Db      7 LLG-LLSHCTGSVTSYVLTQPPSVSVAPGKTASITCGGNNIGSKSVHWYQQKPGQAPVLV 65

Qy     67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCQVWDRASDHPVFGGGTRVT 126
            |||||||||||||||||||||||||:|| || |||||||||||  :|| ||||||:::|
Db     66 VYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYCQVWDSSSD-VVFGGGTKLT 124

Qy    127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTP 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTP 184

Qy    187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
            |||||||||||||||||||||||||||||||||||||||||||||||
Db    185 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 232


RESULT 2
S25747
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25747
R;Combriato, G.; Klobeck, H.G.
  Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25747
A;Status: preliminary; translation not shown
```

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A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57812; NID:g33723; PIDN:CAA40949.1; PID:g33724
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match          81.5%;     Score 1012.5;   DB 2;   Length 233;
Best Local Similarity 85.1%;    Pred. No. 1.5e-60;
Matches  194;   Conservative  13;   Mismatches  20;   Indels  1;   Gaps  1;

Qy-    7 LLGLILLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV 66
         |||  ||  :| :|||||||||||||||||||||| :::||||||| ::|
Db     7 LLG--LLSHCTGSVTSYVLTQPPSVSVSVAPGKAARITCGGINIASKSVHWYQQKPGQAPVLV 65

Qy    67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT 126
         :| ||||||||||||||||||||||||||  ||||||||||||||||| :||| :|
Db    66 VYGDSDRPSGIPERFSGSNSGNTATLNISRVEAGDEAAYYCQVWDSSSDHVVFGGGTKLT 125

Qy   127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 185

Qy   187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   186 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 3
S25738
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Accession: S25738
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25738
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-231 <COM>
A;Cross-references: EMBL:X57802; NID:g33701; PIDN:CAA40940.1; PID:g33702
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;146-214/Domain: immunoglobulin homology <IMM>

Query Match          78.8%;     Score 979;   DB 2;   Length 231;
Best Local Similarity 80.3%;    Pred. No. 2.5e-58;
Matches  187;   Conservative  13;   Mismatches  21;   Indels  12;   Gaps  2;

Qy    12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
         |:::|        :  :|||||||||||||||| :|:|
Db     1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGQTASITCSGDTLGDKYACWTQQKPGH 60

Qy    62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
         :|:||| ::|| ||||||||||||||||||||| :| |||||||||| |    :||||
Db    61 SPVLIVFQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWD--SSTAVFGG 118

Qy   122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
         ||::||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 GTKLTVLSQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy   182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231

RESULT 4
S25751
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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C;Accession: S25751
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25751
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-231 <COM>
A;Cross-references: EMBL:X57816; NID:g33731; PIDN:CAA40953.1; PID:g33732
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;146-214/Domain: immunoglobulin homology <IMM>

Query Match          77.2%;     Score 959;   DB 2;   Length 231;
Best Local Similarity 79.0%;    Pred. No. 5.3e-57;
Matches  184;   Conservative  14;   Mismatches  23;   Indels  12;   Gaps  2;

Qy    12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
         |:::|        :  :|||||||||||||| :|:|
Db     1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGKTASITCSGDKLGDKYASWYQQKAGQ 60

Qy    62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
         :|:||| :|| ||||||||||||||||||||| :| |||||||||| |    :||||
Db    61 SPVLIVYRHSKRPSGIPERFSGSNSGNTATLTISGTQVMDEADYYCQAWD--SSIVVFGG 118

Qy   122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
         ||::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy   182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231

RESULT 5
S25753
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25753
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25753
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-231 <COM>
A;Cross-references: EMBL:X57818; NID:g33735; PIDN:CAA40955.1; PID:g33736
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;146-214/Domain: immunoglobulin homology <IMM>

Query Match          77.2%;     Score 959;   DB 2;   Length 231;
Best Local Similarity 78.5%;    Pred. No. 5.3e-57;
Matches  183;   Conservative  17;   Mismatches  21;   Indels  12;   Gaps  2;

Qy    12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
         |:::|        :  :|||||||||||||| :|:|
Db     1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGQTASITCFGDKLGSSWYQQKPGQ 60

Qy    62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
         :|::| : :|| ||||||||||||||||||||| :| ||:||||||| |    :||||
Db    61 SPVLVYQDTNRPSGIPERFSGSNSGNTATLTISETQAMDEGDYYCQAWD--SNTVVFGG 118

Qy   122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
         ||::||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 GTKLTVLSQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy   182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231
```

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: October 2, 2003, 08:56:23 ; Search time 6.45442 seconds
                                        (without alignments)
                                        1704.917 Million cell updates/sec

Title: US-09-758-173-2
Perfect score: 1243
Sequence: 1 MRVPAQLLGLLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Match	Query Length	DB	ID	AC	Description
1	548	44.1	105	1	LAC_HUMAN	P01842	homo sapien
2	522	42.0	213	1	I1L1_HUMAN	P15814	homo sapien
3	472	38.0	111	1	LV3B_HUMAN	P80748	homo sapien
4	444	35.7	108	1	LV5A_HUMAN	P01719	homo sapien
5	417	33.5	107	1	LV4C_HUMAN	P01717	homo sapien
6	415	33.4	105	1	LAC_PIG	P01846	sus scrofa
7	412	33.1	105	1	LAC1_MOUSE	P01843	mus musculu
8	407	32.7	106	1	LV4A_HUMAN	P01715	mus musculu
9	400	32.2	111	1	LV7A_HUMAN	P01720	homo sapien
10	399	32.1	105	1	LAC_RABIT	P01847	oryctolagus
11	399	32.1	106	1	LV4B_HUMAN	P01716	homo sapien
12	397	31.9	106	1	LV4E_HUMAN	P06889	homo sapien
13	385.5	31.0	104	1	LAC1_RAT	P20766	rattus norv
14	380.5	30.6	104	1	LAC2_RAT	P20767	rattus norv
15	378	30.4	106	1	LV4D_HUMAN	P01718	homo sapien
16	377	30.3	105	1	LAC5_MOUSE	P20765	mus spretus
17	374.5	30.1	104	1	LAC3_MOUSE	P01845	mus musculu
18	369.5	29.7	104	1	LAC2_MOUSE	P01844	mus musculu
19	368	29.6	130	1	LV1G_HUMAN	P06316	homo sapien
20	360	29.0	108	1	LV3A_HUMAN	P01714	homo sapien
21	357	28.7	111	1	LV1D_HUMAN	P01702	homo sapien
22	347	27.9	105	1	LAC5_MOUSE	P20764	mus musculu
23	342	27.5	111	1	LV1C_HUMAN	P01701	homo sapien
24	331	26.6	111	1	LV6C_HUMAN	P06317	homo sapien
25	328	26.4	109	1	LV1I_HUMAN	P06888	homo sapien
26	327	26.3	111	1	LV2G_HUMAN	P01710	homo sapien
27	326.5	26.3	103	1	LAC_CHICK	P20763	gallus gall
28	326.5	26.3	112	1	LV1B_HUMAN	P01700	homo sapien
29	325.5	26.2	112	1	LV2K_HUMAN	P04209	homo sapien
30	325	26.1	111	1	LV1A_HUMAN	P01699	homo sapien
31	322.5	25.9	112	1	LV6A_HUMAN	P01721	homo sapien
32	320.5	25.8	117	1	LV1J_HUMAN	P01602	homo sapien
33	318.5	25.6	129	1	KV1W_HUMAN	P04431	homo sapien
34	318	25.6	111	1	LV2F_HUMAN	P01709	homo sapien
35	314.5	25.3	131	1	LV6E_HUMAN	P06319	homo sapien
36	313	25.2	109	1	LV1F_HUMAN	P04208	homo sapien
37	313	25.2	111	1	LV2C_HUMAN	P01706	homo sapien
38	310.5	25.0	112	1	LV1H_HUMAN	P06887	homo sapien
39	310	24.9	109	1	LV2E_HUMAN	P01708	homo sapien
40	310	24.9	111	1	LV2I_HUMAN	P01712	homo sapien
41	303	24.4	111	1	LV2A_HUMAN	P01704	homo sapien
42	302	24.3	111	1	LV2B_HUMAN	P01705	homo sapien
43	298.5	24.0	129	1	KV1X_HUMAN	P04432	homo sapien
44	298	24.0	111	1	LV2D_HUMAN	P01707	homo sapien
45	298	24.0	113	1	LV1_CHICK	P04210	gallus gall

ALIGNMENTS

RESULT 1
LAC_HUMAN
ID   LAC_HUMAN   STANDARD;   PRT;   105 AA.
AC   P01842; P80423;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain C regions.
GN   IGLC1 AND IGLC2 AND IGLC3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (BENCE-JONES PROTEIN SH).
RX   MEDLINE=70166723; PubMed=4909564;
RA   Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT   complete amino acid sequence and the location of the disulfide
RT   bridges.";
RL   J. Biol. Chem. 245:2171-2176(1970).
RN   [2]
RP   SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RX   MEDLINE=69088880; PubMed=4883841;
RA   Milstein C., Clegg J.B., Jarvis J.M.;
RT   "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT   Bence-Jones protein.";
RL   Biochem. J. 110:631-652(1968).
RN   [3]
RP   SEQUENCE (BENCE-JONES PROTEIN NIG-64).
RX   MEDLINE=8186114; PubMed=6404900;
RA   Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA   Shimizu A.;
RT   "Comparative studies on the structure of the light chains of human
RT   immunoglobulins.IV. Assignment of a subsubgroup.";
RL   J. Biochem. 93:421-429(1983).
RN   [4]
RP   SEQUENCE (BENCE-JONES PROTEIN KERN).
RX   MEDLINE=71150336; PubMed=5549568;
RA   Ponstingl H., Hess M., Hilschmann N.;
RT   "Structural rule of antibodies. Primary structure of a monoclonal
RT   immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
RT   protein Kern). V. The complete amino acid sequence and its genetic
RT   interpretation.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
RN   [5]
RP   PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
RX   MEDLINE=74109253; PubMed=4814727;
RA   Chen B.L., Poljak R.J.;
RT   "Amino acid sequence of the (lambda) light chain of a human myeloma
RT   immunoglobulin (IgG New).";
RL   Biochemistry 13:1295-1302(1974).
RN   [6]
RP   SEQUENCE (DOT).
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;

```
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
RX   MEDLINE=75046825; PubMed=4215080;
RA   Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
RA   Saul F.;
RT   "The three-dimensional structure of the fab' fragment of a human
RT   myeloma immunoglobulin at 2.0-A resolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
RN   [8]
RP   PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
RX   MEDLINE=75013804; PubMed=4415202;
RA   Fett J.W., Deutsch H.F.;
RT   "Primary structure of the Mcg lambda chain.";
RL   Biochemistry 13:4102-4114(1974).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
RA   Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA   Panagiotopoulos N.;
RT   "Rotational allomerism and divergent evolution of domains in
RT   immunoglobulin light chains.";
RL   Biochemistry 14:3953-3961(1975).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY OF MCG.
RX   MEDLINE=90113913; PubMed=2515285;
RA   Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT   "Three-dimensional structure of a light chain dimer crystallized in
RT   water. Conformational flexibility of a molecule in two crystal
RT   forms.";
RL   J. Mol. Biol. 210:601-615(1989).
RN   [11]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82080680; PubMed=6273747;
RA   Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
RT   "Clustered arrangement of immunoglobulin lambda constant region genes
RT   in man.";
RL   Nature 294:536-540(1981).
CC   -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN
CC       FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE
CC       KERN+ MARKER, THE NEWM PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN
CC       HAS THE KERN+ MARKER, AND THE MCG+ MARKER.
CC   -!- MISCELLANEOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE
CC       3 MOST 5' WERE SEQUENCED. THESE CORRSPOND TO THE MCG SEQUENCE
CC       (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
CC       SEQUENCE (LAMBDA-3).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   --------------------------------------------------------------------------
```
```
DR   EMBL; J00253; AAA59107.1; -.
DR   EMBL; L38562; AAB36581.1; ALT_INIT.
DR   EMBL; X51754; CAB38569.1; ALT_INIT.
DR   EMBL; X51755; CAA36049.1; -.
DR   EMBL; X51755; CAA36051.1; -.
DR   PIR; A92057; L2HU.
DR   PDB; 2MCG; 15-JUL-92.
DR   PDB; 7FAB; 31-JAN-94.
DR   PDB; 1AQK; 04-FEB-98.
DR   PDB; 1LIL; 15-MAY-97.
DR   Genew; HGNC:5855; IGLC1.
DR   Genew; HGNC:5856; IGLC2.
DR   Genew; HGNC:5857; IGLC3.
DR   MIM; 147220; -.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
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DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Bence-Jones protein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        6    100       IG-LIKE.
FT   DISULFID     27     86
FT   DISULFID    104    104       INTERCHAIN (WITH HEAVY CHAIN).
FT   VARIANT       5      5       A -> N (IN MCG+ MARKER).
FT                                /FTId=VAR_003898.
FT   VARIANT       7      7       S -> T (IN MCG+ MARKER).
FT                                /FTId=VAR_003899.
FT   VARIANT      45     45       S -> G (IN KERN+ MARKER).
FT                                /FTId=VAR_003900.
FT   VARIANT      56     56       T -> K (IN MCG+ MARKER).
FT                                /FTId=VAR_003901.
FT   VARIANT      82     82       R -> K (IN OZ+ MARKER).
FT                                /FTId=VAR_003902.
FT   STRAND        8     11
FT   HELIX        15     19
FT   TURN         20     21
FT   STRAND       24     32
FT   STRAND       38     43
FT   TURN         44     45
FT   STRAND       46     48
FT   STRAND       52     59
FT   TURN         61     62
FT   STRAND       65     72
FT   HELIX        75     80
FT   STRAND       84     89
FT   STRAND       94     99
SQ   SEQUENCE   105 AA;  11236 MW;  DCD9C7C201C13CC2 CRC64;

Query Match             44.1%;  Score 548;  DB 1;  Length 105;
Best Local Similarity   100.0%;  Pred. No. 7.6e-37;
Matches  105   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy        130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 189
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 60

Qy        190 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
              |||||||||||||||||||||||||||||||||||||||||||||
Db         61 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 105
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RESULT 2
ILL1_HUMAN

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ID   ILL1_HUMAN     STANDARD;      PRT;    213 AA.
AC   P15814;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-
DE   related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
DE   (CD179b antigen).
GN   IGLL1 OR IGL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89315835; PubMed=2501791;
RA   Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
RA   McKearn J.P.;
RT   "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
RT   expressed in pre-B cells and may encode the human immunoglobulin
```

```
               GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October 2, 2003, 08:56:23 ; Search time 22.6452 Seconds
                                        (without alignments)
                                        2666.544 Million cell updates/sec

Title:             US-09-758-173-2
Perfect score:     1243
Sequence:          1 MRVPAQLLGLLLLWLPGARC........CQVTHEGSTVEKTVAPTECS 234

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:     830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_23:*
                  1: sp_archea:*
                  2: sp_bacteria:*
                  3: sp_fungi:*
                  4: sp_human:*
                  5: sp_invertebrate:*
                  6: sp_mammal:*
                  7: sp_mhc:*
                  8: sp_organelle:*
                  9: sp_phage:*
                 10: sp_plant:*
                 11: sp_rodent:*
                 12: sp_virus:*
                 13: sp_vertebrate:*
                 14: sp_unclassified:*
                 15: sp_rvirus:*
                 16: sp_bacteriap:*
                 17: sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1037	83.4	234	4	Q8N355	Q8N355 homo sapien
2	981	78.9	233	4	Q8TBC9	Q8TBC9 homo sapien
3	961	77.3	233	4	Q8N5F4	Q8N5F4 homo sapien
4	917.5	73.8	233	4	Q96I69	Q96I69 homo sapien
5	885	71.2	237	4	Q8WUK4	Q8WUK4 homo sapien
6	884.5	71.2	236	4	Q8NEJ1	Q8NEJ1 homo sapien
7	883	71.0	237	4	Q8WTU6	Q8WTU6 homo sapien
8	856.5	68.9	236	4	Q96E61	Q96E61 homo sapien
9	763	61.4	240	4	Q8WUK3	Q8WUK3 homo sapien
10	700	56.3	235	11	Q99M11	Q99M11 mus musculu
11	551	44.3	106	4	Q8TCJ5	Q8TCJ5 homo sapien
12	479.5	38.6	234	11	Q8VCP0	Q8VCP0 mus musculu
13	474.5	38.2	234	4	Q8NEK1	Q8NEK1 homo sapien
14	468.5	37.7	130	11	Q9D8W4	Q9D8W4 mus musculu
15	466	37.5	239	4	Q8NEK0	Q8NEK0 homo sapien
16	464	37.3	239	4	Q8TCD0	Q8TCD0 homo sapien
17	462.5	37.2	238	11	Q8VCI6	Q8VCI6 mus musculu
18	449.5	36.2	234	11	Q8R062	Q8R062 mus musculu
19	444	35.7	235	11	Q91W12	Q91W12 mus musculu
20	441.5	35.5	238	11	Q99M37	Q99M37 mus musculu
21	432.5	34.8	234	11	Q91WF8	Q91WF8 mus musculu
22	431.5	34.7	233	11	Q91WS9	Q91WS9 mus musculu
23	423	34.0	239	11	Q8VC55	Q8VC55 mus musculu
24	398.5	32.1	214	11	Q9R1A5	Q9R1A5 mus musculu
25	395.5	31.8	234	11	Q8R028	Q8R028 mus musculu
26	394	31.7	239	11	Q8K0F8	Q8K0F8 mus musculu
27	382	30.7	107	4	Q9NSD6	Q9NSD6 homo sapien
28	376.5	30.3	107	4	Q9UL82	Q9UL82 homo sapien
29	375.5	30.2	105	11	Q99JC1	Q99JC1 mus musculu
30	347	27.9	110	4	Q8TE63	Q8TE63 homo sapien
31	338	27.2	116	4	Q96JD0	Q96JD0 homo sapien
32	315.5	25.4	112	4	Q96JD1	Q96JD1 homo sapien
33	314	25.3	112	4	Q96JD2	Q96JD2 homo sapien
34	310	24.9	101	4	Q8IZD8	Q8IZD8 homo sapien
35	289	23.3	108	4	Q96SB0	Q96SB0 homo sapien
36	273.5	22.0	684	13	Q90544	Q90544 ginglymosto
37	264.5	21.3	127	11	Q925S9	Q925S9 mus musculu
38	260.5	21.0	112	13	Q8KIF0	Q8KIF0 ginglymosto
39	252	20.3	257	13	Q90536	Q90536 ginglymosto
40	250	20.1	268	13	Q90524	Q90524 ginglymosto
41	250	20.1	471	4	Q8TC77	Q8TC77 homo sapien
42	245	19.7	106	5	Q9U410	Q9U410 schistosoma
43	244.5	19.7	112	11	Q8KIF2	Q8KIF2 mus musculu
44	244.5	19.7	134	11	Q8VDD0	Q8VDD0 mus musculu
45	244	19.6	113	11	Q8CGS1	Q8CGS1 mus musculu

ALIGNMENTS

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RESULT 1
Q8N355
ID   Q8N355      PRELIMINARY;     PRT;   234 AA.
AC   Q8N355;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC028090; AAH28090.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  24792 MW;  CC848CAEBA4A9D63 CRC64;

Query Match             83.4%;  Score 1037;  DB 4;  Length 234;
Best Local Similarity   86.5%;  Pred. No. 6.6e-83;
Matches  198;  Conservative   15;  Mismatches   14;  Indels    2;  Gaps    2;

Qy          7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV 66
              |||.|| |||||| | |||::| ||||||||||||||||:||:::::::::::::: ::
Db          7 LLG-LLSHCTGSVTSYVLTQPPSVLTQPPSVSVAPGQTARITCGGNNYGSKSVHWYQQKPGQAPVLV 65
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Qy    67  IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHP-VFGGGTRV  125
          :||||||||||||||||| ||:||||| |:||||||:||||| ::|||   ::|||:||
Db    66  VYDDSDRPSGIPERFSGSNSGNTATLTISRVDAGDEADYYCQLWDSSSDHPVVFGGGTKL  125

Qy   126  TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT  185
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126  TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT  185

Qy   186  PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
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RESULT 2
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Q8TBC9
ID   Q8TBC9;          PRELIMINARY;      PRT;      233 AA.
AC   Q8TBC9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC02823; AAH22823.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;   24867 MW;   367411BFD6F4DF92 CRC64;
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Query Match   78.9%;  Score 981;  DB 4;  Length 233;
Best Local Similarity   79.4%;  Pred. No. 5.3e-78;
Matches  185;  Conservative  17;  Mismatches  21;  Indels  10;  Gaps  1;

Qy    12  LIWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSREYVHWYQQKPAR   61
          : :|:|        | : :|||||||||||||||||||| ||  :|||||| |||||||
Db     1  MAWIPLLLPLLTCTGSEASYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQ   60

Qy    62  APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG  121
          || ||||||||||||||||| ||:||||||| || :|||||||| |:|: :|||  ||||
Db    61  APVLVIYKDNERPSGIPERFSGSSGTTVTLTIISGVQAEDEADYYCQSADSSGTIWVFGG  120

Qy   122  GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV  181
          || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV  180

Qy   182  ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  233
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RESULT 3
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Q8N5F4
ID   Q8N5F4;          PRELIMINARY;      PRT;      233 AA.
AC   Q8N5F4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, and Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032452; AAH32452.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;   24961 MW;   F092CFB6AA6E3A9A CRC64;
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Query Match   77.3%;  Score 961;  DB 4;  Length 233;
Best Local Similarity   80.3%;  Pred. No. 3e-76;
Matches  183;  Conservative  16;  Mismatches  29;  Indels  0;  Gaps  0;

Qy     7  LLGLLILWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSREYVHWYQQKPARAPILV   66
          || ||: : ::       :|||||||||||||||||||||   : :|||||   : |:||
Db     6  LLLPLIIFCTVSEASYELTQPPSVSVSPGQTARITCSGDALPKKIAYWYQQKSGQIPVLV   65

Qy    67  IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT  126
          |||||||||||||||| ||:||||| |:||||||:||||| ::|||    :|||:  :|
Db    66  IYDDTERPSGIPERFSGSSSGTVATL/TLSGAVEDEADYYCYSSDSSGNHWVFGGGTKLT  125

Qy   127  VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP  186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126  VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP  185

Qy   187  SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
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Db   186  SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  233
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RESULT 4
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Q96I69
ID   Q96I69;          PRELIMINARY;      PRT;      233 AA.
AC   Q96I69;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC007782; AAH07782.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;   24802 MW;   C694F8397B27650B CRC64;
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Query Match   73.8%;  Score 917.5;  DB 4;  Length 233;
Best Local Similarity   78.1%;  Pred. No. 1.9e-72;
Matches  178;  Conservative  17;  Mismatches  32;  Indels  17;  Gaps  1;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:12:09 ; Search time 10.3927 Seconds
(without alignments)
952.662 Million cell updates/sec

Title: US-09-758-173-2
Perfect score: 1243
Sequence: 1 MRVPAQLLGLLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1243	100.0	234	3	US-08-487-550-2	Sequence 2, Appli
2	1243	100.0	234	3	US-09-526-098-2	Sequence 2, Appli
3	1015.5	81.7	233	3	US-08-523-894-6	Sequence 6, Appli
4	973	78.3	236	4	US-08-487-550-10	Sequence 10, Appli
5	973	78.3	236	4	US-09-526-098-10	Sequence 10, Appli
6	886	71.3	234	4	US-09-372-425A-4	Sequence 4, Appli
7	880.5	70.8	236	3	US-09-049-672A-7	Sequence 7, Appli
8	867.5	69.8	235	3	US-09-049-672A-10	Sequence 10, Appli
9	861	69.3	235	2	US-08-378-939-12	Sequence 12, Appli
10	855.5	69.3	238	4	US-08-793-450-6	Sequence 6, Appli
11	855	68.8	235	3	US-09-049-672A-12	Sequence 12, Appli
12	844	67.9	240	3	US-09-049-672A-11	Sequence 11, Appli
13	812	65.3	235	4	US-09-152-060-70	Sequence 70, Appli
14	809	65.1	235	4	US-09-152-060-88	Sequence 88, Appli
15	658.5	53.0	229	3	US-08-751-359-22	Sequence 22, Appli
16	658.5	53.0	229	3	US-08-907-146-22	Sequence 22, Appli
17	567	45.6	109	2	US-08-761-277A-51	Sequence 51, Appli
18	560.5	45.1	200	6	5189147-10	Patent No. 5189147
19	548	44.1	105	1	US-08-422-101-9	Sequence 9, Appli
20	548	44.1	105	2	US-08-422-091-9	Sequence 9, Appli
21	548	44.1	105	2	US-08-422-092-9	Sequence 9, Appli
22	548	44.1	105	3	US-08-788-800-6	Sequence 6, Appli
23	548	44.1	105	3	US-08-422-093-9	Sequence 9, Appli
24	543	43.7	105	4	US-08-422-112-9	Sequence 9, Appli
25	543	43.7	106	4	US-09-313-942-14	Sequence 14, Appl
26	535	43.0	104	4	US-09-025-769B-170	Sequence 170, Appl
27	503	40.5	241	2	US-07-916-098A-56	Sequence 56, Appl

28	502.5	40.4	235	3	US-08-812-586-16	Sequence 16, Appl
29	502.5	40.4	235	4	US-09-535-832A-17	Sequence 8, Appl
30	500.5	40.3	143	2	US-08-345-321-8	Sequence 5, Appli
31	500.5	40.3	236	1	US-08-157-101A-5	Sequence 26, Appli
32	496	39.9	234	4	US-09-740-002-26	Sequence 24, Appl
33	494.5	39.8	234	4	US-09-740-002-24	Sequence 20, Appl
34	492	39.6	242	4	US-09-479-614-20	Sequence 153, App
35	487	39.2	235	1	US-08-276-852-153	Sequence 153, App
36	487	39.2	235	1	US-08-899-575-153	Sequence 153, App
37	487	39.2	235	1	US-08-899-575-153	Sequence 153, App
38	487	39.2	235	5	PCT-US95-08743-153	Sequence 4, Appli
39	483.5	38.9	234	5	PCT-US94-07659-4	Sequence 2, Appli
40	477.5	38.4	234	2	US-07-690-192-2	Sequence 6, Appli
41	475	38.2	239	3	US-08-487-550-6	Sequence 6, Appli
42	475	38.2	239	4	US-09-526-098-6	Sequence 6, Appli
43	469.5	37.8	234	3	US-09-049-672A-6	Sequence 110, App
44	467.5	37.6	128	1	US-08-478-039-110	Sequence 110, App
45	467.5	37.6	128	1	US-08-476-349A-110	

ALIGNMENTS

RESULT 1
US-08-487-550-2
; Sequence 2, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
 APPLICANT: Anderson, Darrell R.
 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
 TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
 TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 TITLE OF INVENTION: IMUNOSUPPRESANTS"
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,550
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-131
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-836-6620
 TELEFAX: 703-836-2021
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 234 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
US-08-487-550-2

Query Match 100.0%; Score 1243; DB 3; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.2e-102;
Matches 234; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

Qy 1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60

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Qy   61  RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG  120
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Db   61  RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG  120

Qy  121  GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG  180
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Db  121  GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG  180

Qy  181  VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
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RESULT 2
US-09-526-098-2
; Sequence 2, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/526,098
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 234 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-526-098-2

Query Match   100.0%; Score 1243; DB 4; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.2e-102;
Matches 234; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy  121  GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG  180
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Db  121  GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG  180

Qy  181  VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
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Db  181  VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
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RESULT 3
US-08-523-894-6
; Sequence 6, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
;   APPLICANT: Hanna, Nabil
;   APPLICANT: Newman, Roland A.
;   APPLICANT: Reff, Mitchell E.
;   TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;   TITLE OF INVENTION: Therapy
;   NUMBER OF SEQUENCES: 59
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314-3187
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/523,894
;   FILING DATE: 06-SEP-1995
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-165
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 233 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-523-894-6

Query Match   81.7%; Score 1015.5; DB 3; Length 233;
Best Local Similarity   86.0%; Pred. No. 1.7e-82;
Matches 196; Conservative   10; Mismatches   21; Indels   1; Gaps   1;

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Qy   67  IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT  126
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Qy  127  VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP  186
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Qy  187  SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
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RESULT 4
US-08-487-550-10

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October  2, 2003, 09:18:44 ; Search time 87.8457 Seconds
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Title:            US-09-758-173-2
Perfect score:    1243
Sequence:         1 MRVPAQLLGLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 234

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters:     587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
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   18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1243	100.0	234	10	US-09-948-429B-2	Sequence 2, Appli
2	1243	100.0	234	12	US-10-124-807-2	Sequence 2, Appli
3	1243	100.0	234	12	US-10-291-532-2	Sequence 2, Appli
4	1243	100.0	234	14	US-10-124-905-2	Sequence 2, Appli
5	1015.5	81.7	233	15	US-10-211-357-6	Sequence 6, Appli
6	1009	81.2	214	11	US-09-972-656-96	Sequence 96, Appl
7	1001	80.5	232	12	US-10-225-108A-12	Sequence 10, Appl
8	973	78.3	236	10	US-09-948-429B-10	Sequence 10, Appl
9	973	78.3	236	12	US-10-124-807-10	Sequence 10, Appl
10	973	78.3	236	12	US-10-291-532-10	Sequence 10, Appl
11	973	78.3	236	14	US-10-124-905-10	Sequence 10, Appl
12	944	75.9	218	10	US-09-791-153A-51	Sequence 51, Appl
13	936.5	75.3	244	9	US-09-925-301-1424	Sequence 1424, AP
14	932	75.0	212	11	US-09-972-656-98	Sequence 98, Appl
15	914.5	73.6	229	12	US-10-310-719-36	Sequence 36, Appl
16	890	71.6	242	12	US-10-225-108A-14	Sequence 14, Appl
17	882	71.0	218	11	US-09-972-656-102	Sequence 102, App
18	881	70.9	234	12	US-10-194-801C-4	Sequence 4, Appli
19	880	70.8	235	10	US-09-747-669-6	Sequence 6, Appli
20	880	70.8	235	15	US-10-290-703-6	Sequence 202, App
21	873.5	70.3	221	14	US-10-001-857-202	Sequence 88, Appl
22	870.5	70.0	217	11	US-09-972-656-88	Sequence 14, Appl
23	865.5	69.6	219	10	US-09-974-449-38	Sequence 38, Appl
24	857	68.9	216	11	US-09-972-655-90	Sequence 90, Appl
25	856.5	68.9	219	15	US-10-026-925-57	Sequence 57, Appl
26	854	68.7	216	12	US-09-972-655-108	Sequence 108, App
27	816	65.6	235	12	US-10-076-747-82	Sequence 82, Appl
28	812	65.3	235	9	US-09-853-161-70	Sequence 70, Appl
29	812	65.3	235	9	US-09-852-659A-70	Sequence 70, Appl
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32	809	65.1	235	9	US-09-852-659A-88	Sequence 19, Appl
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34	804	64.7	216	10	US-09-736-371B-19	Sequence 26, Appl
35	803.5	64.6	239	15	US-10-221-945-2	Sequence 49, Appl
36	749	60.3	239	10	US-09-828-995B-26	Sequence 8, Appli
37	746.5	60.1	246	11	US-09-909-567B-49	Sequence 7, Appli
38	691.5	55.6	216	9	US-09-291-299A-8	Sequence 10, Appl
39	665	53.5	217	9	US-09-291-299A-7	Sequence 9, Appli
40	646.5	52.0	216	9	US-09-291-299A-10	Sequence 901, App
41	637.5	51.3	216	9	US-09-291-299A-9	Sequence 901, App
42	631	50.8	139	10	US-09-796-692-901	Sequence 742, App
43	631	50.8	139	15	US-10-040-862-901	Sequence 742, App
44	616	49.6	143	10	US-09-796-692-742	
45	616	49.6	143	15	US-10-040-862-742	

ALIGNMENTS

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RESULT 1
US-09-948-429B-2
; Sequence 2, Application US/09948429B
; Patent No. US20020177689A1
GENERAL INFORMATION:
   APPLICANT:  Anderson, Darrell R.
   TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
   TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
   TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
   TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
   NUMBER OF SEQUENCES:  12
   CORRESPONDENCE ADDRESS:
      ADDRESSE:  BURNS, DOANE, SWECKER & MATHIS
      STRET:  699 Prince Street
      CITY:  Alexandria
      STATE:  VA
      COUNTRY:  USA
      ZIP:  22314
   COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/948,429B
      FILING DATE:
      CLASSIFICATION:
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  09/383,916
      FILING DATE:
      APPLICATION NUMBER:  US 08/487,550
      FILING DATE:  07-JUN-1995
   ATTORNEY/AGENT INFORMATION:
      NAME:  Teskin, Robin L.
      REGISTRATION NUMBER:  35,030
      REFERENCE/DOCKET NUMBER:  012712-131
   TELECOMMUNICATION INFORMATION:
      TELEPHONE:  703-836-6620
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;    TELEFAX:   703-836-2021
;  INFORMATION FOR SEQ ID NO:   2:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 234 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-09-948-429B-2

Query Match     100.0%;   Score 1243;  DB 10;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 4.8e-92;
Matches 234;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCQVWDRASDHPVFG 120
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 2
US-10-124-807-2
; Sequence 2, Application US/10124807
; Publication No. US2003016 5207A1
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314
;   COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/10/124,807
;    FILING DATE:
;    CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 09/383,916
;    FILING DATE:
;    APPLICATION NUMBER: US 08/487,550
;    FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
;    TELEFAX: 703-836-2021
;   INFORMATION FOR SEQ ID NO: 2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 234 amino acids
;     TYPE: amino acid
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;    TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-10-124-807-2

Query Match     100.0%;   Score 1243;  DB 12;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 4.8e-92;
Matches 234;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCQVWDRASDHPVFG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCQVWDRASDHPVFG 120

Qy  121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
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RESULT 3
US-10-291-532-2
; Sequence 2, Application US/10291532
; Publication No. US20030180290A1
; GENERAL INFORMATION:
;   APPLICANT: HARIHARAN, KANDASAMY
;   APPLICANT: HANNA, NABIL
;   TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
;   TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
;   TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
;   FILE REFERENCE: 037003/291872
;   CURRENT APPLICATION NUMBER: US/10/291,532
;   CURRENT FILING DATE: 2002-11-12
;   PRIOR APPLICATION NUMBER: 60/331,187
;   PRIOR FILING DATE: 2001-11-09
;   PRIOR APPLICATION NUMBER: 09/758,173
;   PRIOR FILING DATE: 2001-01-12
;   PRIOR APPLICATION NUMBER: 09/383,916
;   PRIOR FILING DATE: 1999-08-26
;   PRIOR APPLICATION NUMBER: 08/487,950
;   PRIOR FILING DATE: 1995-06-07
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: primatized peptide sequence
US-10-291-532-2
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Query Match     100.0%;   Score 1243;  DB 12;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 4.8e-92;
Matches 234;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:01:50 ; Search time 3758.85 Seconds
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Perfect score: 1431
Sequence: 1 ATGAAACACCTGTGGTTCTT........CCCTGTCTCCGGGTAAATGA 1431

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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        14: gb_vi:*
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        18: em_in:*
        19: em_mu:*
        20: em_om:*
        21: em_or:*
        22: em_ov:*
        23: em_pat:*
        24: em_ph:*
        25: em_pl:*
        26: em_ro:*
        27: em_sts:*
        28: em_un:*
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        31: em_htg_inv:*
        32: em_htg_other:*
        33: em_htg_mus:*
        34: em_htg_pln:*
        35: em_htg_rod:*
        36: em_htg_mam:*
        37: em_htg_vrt:*
        38: em_sy:*
        39: em_htgo_hum:*
        40: em_htgo_mus:*
        41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	1315.8	91.9	1431	6	AR108867	AR108867 Sequence
5	1315.8	91.9	1431	6	AR265201	AR265201 Sequence
6	1314.2	91.8	1431	6	BD063039	BD063039 Identific
7	1237.2	86.5	1431	6	E10697	E10697 cDNA encodi
8	1234.8	86.3	1567	6	AR135359	AR135359 Sequence
9	1227.6	85.8	1596	9	AK098516	AK098516 Homo sapi
10	1221.6	85.4	1418	9	A49389	A49389 Sequence 7
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14	1171.4	81.8	1404	6	AR135375	AR135375 Sequence
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17	1166.6	81.5	1404	6	AR135376	AR135376 Sequence
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19	1125.8	78.7	1633	9	AK097859	AK097859 Homo sapi
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21	1123.6	78.5	1428	6	AR031184	AR031184 Sequence
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28	1117.4	78.1	1679	9	BC018747	BC018747 Homo sapi
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32	1116.2	78.0	1624	9	Y14735	Y14735 Homo sapien
33	1115.4	77.9	1630	9	BC024289	BC024289 Homo sapi
34	1113.2	77.8	1673	9	Y14737	Y14737 Homo sapien
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ALIGNMENTS

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DEFINITION Sequence 3 from patent US 6113898.
ACCESSION   AR108863
VERSION   AR108863.1 GI:12825139
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1431)
  AUTHORS   Anderson.D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
  TITLE   Human B7.1-specific primatized antibodies and transfectomas
            expressing said antibodies
  JOURNAL   Patent: US 6113898-A 3 05-SEP-2000;

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FEATURES             Location/Qualifiers
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BASE COUNT       322 a    469 c    380 g    260 t
ORIGIN

Query Match      100.0%;  Score 1431;  DB 6;  Length 1431;
Best Local Similarity  100.0%;  Pred. No. 3.6e-278;
Matches 1431;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy  301 CTGAACTTGAATTCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT  360
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DEFINITION  Sequence 3 from patent US 6492134.
ACCESSION   AR265197
VERSION     AR265197.1  GI:29693518
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1431)
  AUTHORS   Aquin,S. and Vezina,Louis.-P.
  TITLE     Method for producing polyhydroxyalkanoates in recombinant organisms
  JOURNAL   Patent: US 6492134-A 3 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1..1431
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BASE COUNT       322 a    469 c    380 g    260 t
ORIGIN

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Best Local Similarity  100.0%;  Pred. No. 3.6e-278;
Matches 1431;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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OM nucleic - nucleic search, using sw model

              GenCore version 5.1.6
              Copyright (c) 1993 - 2003  Compugen Ltd.

Run on:       October  2, 2003, 12:12:30  ; Search time 293.094 Seconds
                                             (without alignments)
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Sequence:     1 ATGAAACACCTGGTTCTT.......CCCGTGTCTCCGGGTAAATGA 1431

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Searched:     2252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:        5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
              Maximum Match 100%
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SUMMARIES

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 No.  Score  Match Length DB  ID                  Description
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   3   1431  100.0  1431  24  AAS17243            DNA sequence of a
   4   1315.8  91.9  1431  18  AAT62513            Primatised anti-hu
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   7   1246.4  87.1  1634  21  AAZ50012            Human immune syste
   8   1237.2  86.5  1431  17  AAT18059            Monoclonal antibod
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                                                          Human immune syste
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  11  1171.4  81.9  1404   18  AAT62868            Human gamma-4PE he
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  13  1166.6  81.5  1404   18  AAT62869            Nucleotide sequenc
  14  1135    79.3  1428   22  AAH74680            Hepatitis C virus
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  16  1125.2  78.6  1428   21  AAT61241            Human immunoglobul
  17  1124.2  78.6  1507   21  AAA09695            cDNA of the heavy
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  25  1113.2  77.8  1644   22  AAS22593            Traget plasmid Man
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  27  1112.2  77.7  6281   22  AAC84206            Human anti-RSV mon
  28  1110.8  77.6  1428   21  AAT61279            Antibody D heavy c
  29  1103.6  77.1  1617   14  AAQ35099            Reshaped CAMPATH-1
  30  1103    77.1  1467   13  AAQ23570            Human benign prost
  31  1102    77.0  1599   24  ABK64550            Colon adenocarcino
  32  1102    77.0  1599   24  ABL62673            Lung cancer relate
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  34  1102    77.0  1599   24  ABL62294            Plasmid Hu19BHcpcd
  35  1100.8  76.9  1427   19  AAV41429            Plasmid Hu19CHcpcd
  36  1100.8  76.9  1427   19  AAV41431            Monoclonal antibod
  37  1098.8  76.8  1449   20  AAX06951            Monoclonal antibod
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  41  1096    76.6  7521   22  AAF30315            Human C5E10 antibo
  42  1094.2  76.5  1407   24  AAD45757            Antibody C5E10 hea
  43  1094.2  76.5  1407   25  AB224021            Encodes heavy chai
  44  1094    76.5  1549   13  AAQ20066            Reshaped CD4 antib
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ALIGNMENTS

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                          DE   Primatised anti-human B7.1 antigen antibody 7C10 heavy chain DNA.
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                          KW   Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
                          KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
                          KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
                          KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
                          KW   type 1 diabetes mellitus; graft versus host disease;
                          KW   hetero-hybridoma; transfectoma; ss.
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                          PR   07-JUN-1995;  95US-0487550.
                          XX
                          PA   (IDEC-) IDEC PHARM CORP.
                          XX
                          PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
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XX
DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01818.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 7; Fig 8B; 81pp; English.
XX
CC   2 DNA sequences (AAT62509 and AAT62510) respectively code for
CC   primatised forms (AAW01817 and AAW01818) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   7C10.  Cloned 7C10 light and heavy variable genes are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells.  Primatised 7B6 and 16C10 anti-B7.1
CC   antibodies have been produced (see also AAW01819-22).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;

Query Match             100.0%;  Score 1431;  DB 18;  Length 1431;
Best Local Similarity   100.0%;
Matches 1431;            Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy   241 AATCCCTCCCTCAAGAGTCGAGTCACCATTCAAAAGACACGTCCAAGAACCAGTTCTTC   300
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Db   241 AATCCCTCCCTCAAGAGTCGAGTCACCATTCAAAAGACACGTCCAAGAACCAGTTCTTC   300

Qy   301 CTGAACTTGAATTCTGTGACCACGGCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT   360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGAACTTGAATTCTGTGACCACGGCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT   360

Qy   361 CGCCCTGATTGCACAACCATTGTTATGGCGGCTGGGTCGATGTCTGGGGCCCGGGGAC   420
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Db   361 CGCCCTGATTGCACAACCATTGTTATGGCGGCTGGGTCGATGTCTGGGGCCCGGGGAGAC   420

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCACCCTC   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCACCCTC   480

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   540

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCGCTGACCAGCGGCGTGCACACCTTCCCG   600
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Db   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCGCTGACCAGCGGCGTGCACACCTTCCCG   600

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC   660
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Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG   720
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Db   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAGCCCAGCAACACCAAGGTG   720

Qy   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA   780
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Db   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA   780

Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAACCCAAGGACACCCTC   840
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Qy   841 ATGATCTCCGGACCCCTGAGGTCACATGCGGTGGTGGTGGACGTGAGCCACGAAGACCCT   900
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Db   841 ATGATCTCCGGACCCCTGAGGTCACATGCGGTGGTGGTGGACGTGAGCCACGAAGACCCT   900

Qy   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   960
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Db   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   960

Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020
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Qy  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080
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Db  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080

Qy  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140
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Qy  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200
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Qy  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260
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Qy  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1320
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Qy  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1380
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Qy  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA          1431
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA          1431
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RESULT 2
AAV35485
ID   AAV35485 standard; DNA; 1431 BP.
XX
AC   AAV35485;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 7C10 heavy chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..1431
FT                  /*tag= a
FT                  /product= 7C10 heavy chain
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              GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        October  2, 2003, 13:05:20 ; Search time 2366.54 Seconds
                                           (without alignments)
                                           14696.420 Million cell updates/sec

Title:          US-09-758-173-3
Perfect score:  1431
sequence:       1 ATGAAACACCTGTGGTTCTT.......CCCTGTCTCCGGGTAAATGA 1431

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters:      45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
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         9: gb_est1:*
        10: gb_est2:*
        11: gb_htc:*
        12: gb_est3:*
        13: gb_est4:*
        14: gb_est5:*
        15: em_estfun:*
        16: em_estom:*
        17: em_gss_hum:*
        18: em_gss_inv:*
        19: em_gss_pln:*
        20: em_gss_vrt:*
        21: em_gss_fun:*
        22: em_gss_mam:*
        23: em_gss_mus:*
        24: em_gss_pro:*
        25: em_gss_rod:*
        26: em_gss_phg:*
        27: em_gss_vrl:*
        28: gb_gss1:*
        29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description			
c	1	944	66.0	1149	13	BX377695	BX377695	BX377695		
c	2	929.6	65.0	1142	13	BX414495	BX414495	BX414495		
c	3	902	63.0	1020	12	BQ062878	BQ062878	AGENCOURT		
c	4	899.2	62.8	1045	13	BX337477	BX337477	BX337477		

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c   5   894.8   62.5   1149   13        BX381020  BX381020  BX381020
c   6   892.6   62.4   1201   13        BX377803  BX377803  BX377803
c   7   891.2   62.3   1201   13        BX439438  BX439438  BX439438
    8   889.8   62.2    902   13        BU146962  BU146962  AGENCOURT
    9   875.8   61.2   1013   13        BX360518  BX360518  BX360518
c  10   867.6   60.6   1200   13        BX415883  BX415883  BX415883
   11     864   60.4    947   13        BQ709771  BQ709771  AGENCOURT
   12   850.4   59.4    958   13        BX706140  BQ706140  AGENCOURT
c  13   849.2   59.3   1093   13        BX428863  BX428863  BX428863
   14   842.4   58.9    926   10        BG755166  BG755166  602711488
   15   834.2   58.3   1096   13        BX415920  BX415920  BX415920
c  16   831.8   58.1   1201   13        BX338493  BX338493  BX338493
   17   831.2   58.1    901   12        BM007892  BM007892  60361 7577
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   19   830.4   58.0    988   13        BQ708857  BQ708857  AGENCOURT
   20   829.4   58.0   1201   13        BX417147  BX417147  BX417147
   21   824.4   57.6   1029   13        BQ063185  BQ063185  AGENCOURT
   22   823.2   57.5   1019   13        BX325650  BX325650  BX325650
c  23   822.8   57.5    887   13        BQ711255  BQ711255  AGENCOURT
   24   822.2   57.5    918   13        BQ708022  BQ708022  AGENCOURT
c  25     818   57.2   1015   13        BX367600  BX367600  BX367600
   26   817.8   57.1    980   13        BX325701  BX325701  BX325701
c  27   815.2   57.0    995   12        BM914540  BM914540  AGENCOURT
   28   811.8   56.7    889   13        BX346909  BX346909  BX346909.
   29     811   56.7   1147   13        BX360330  BX360330  BX360330
c  30     809   56.5   1009   13        BX456658  BX456658  BX456658
   31   808.8   56.5    881   13        BQ711291  BQ711291  AGENCOURT
c  32   807.4   56.4   1200   13        BX456326  BX456326  BX456326
   33     804   56.2    853   13        BX388631  BX388631  BX388631
   34   801.6   56.0    862   13        BX450248  BX450248  BX450248
   35     800   55.9   1031   13        BQ064886  BQ064886  AGENCOURT
   36   799.4   55.9    852   13        BX450232  BX450232  BX450232
c  37   798.4   55.8   1004   13        BX432300  BX432300  BX432300
   38   797.2   55.7    936   13        BQ711727  BQ711727  AGENCOURT
   39     796   55.6    940   13        BQ705928  BQ705928  AGENCOURT
c  40   795.6   55.6   1070   13        BX397632  BX397632  BX397632
   41   795.2   55.5   1152   13        BX339318  BX339318  BX339318
c  42   794.2   55.5   1151   13        BX378450  BX378450  BX378450
   43   792.2   55.4    885   13        BX408117  BX408117  BX408117
c  44   791.2   55.3   1201   13        BX396322  BX396322  BX396322
c  45   788.8   55.1   1201   13        BX439176  BX439176  BX439176
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ALIGNMENTS

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LOCUS       BX377695               1201 bp    mRNA    linear     EST 08-MAY-2003
DEFINITION  BX377695 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CSODI009YJ10 3-PRIME, mRNA sequence.
ACCESSION   BX377695
VERSION     BX377695.1  GI:30439018
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished
COMMENT     Contact: Genóscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web.: www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CSODI009DE05NP1&cluster=7198.r. Contact :
            Feng Liang Email: fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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FEATURES
     source   Faraday Avenue Genoscope sequence ID : CS0DI009DE05NP1.
              Location/Qualifiers
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              /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
              /note="1st strand cDNA was primed with a NotI-oligo(dT)
              primer. Five prime end enriched, double-strand cDNA was
              digested with Not I and cloned into the Not I and EcoR V
              sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT   188 a   296 c   396 g   267 t   54 others
ORIGIN

Query Match   66.0%;   Score 944;   DB 13;   Length 1201;
Best Local Similarity   95.8%;   Pred. No. 8.8e-199;
Matches 991;   Conservative 17;   Mismatches 22;   Indels   4;   Gaps   4;

Qy   398 TCGATGTCTTGGGGCCCGGGAGACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCAT 457
                : :| |||||||||||||||||||| ||||| ||| ||||||||||||||||||||||
Db   1119 TTKACWACTGGGGCCCAGGGAHCTTGTTCACCGTCYTCAGCYTCAACCAAGGGGCCCAT 1060

Qy   458 CGGTCTTCCCCTGCACCCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCT 517
           |||||::||| :||||| :||||||||||||||||||||||:|||||||||||||||
Db   1059 CGGTYTYCCCCC-KGCACCCTCCTCCAAGAGCACCTCTGGGGCACGCGSCCCTGGGCT 1001

Qy   518 GCCTGGTCAAGGACTACTCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGA 577
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Qy   578 CCAGCGGCGGTGCACACCTTCCCGGCTGTGTCCTACAGTCCTCAGGACTCCTACTCCTCAGCA 637
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Db   578 CCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGWCCTCAGGACTCCTACTCCCTCAGCA 882

Qy   638 GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC 697
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Db   881 GCGTGGTGACCGTGCCCTCCAGCAGCTKG-GCACCCAGACCTACATCTGCAACGTGAATC 823

Qy   698 ACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTC 757
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Db   698 ACAAGCCCAGCAACACCAAGGTGGACAAGAGAGCAGAGGTGAACTCAGTCTTGTGACAAAACTC 763

Qy   758 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCC 817
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Db   762 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCC 703

Qy   818 CCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 877
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Db   702 CCCCRAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 643

Qy   878 TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 937
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Qy   938 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA 997
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Db   582 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGCAGCAACACAG-ACGTACCGTGTGGTCA 524

Qy   998 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 1057
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Qy   1058 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1117
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Db   463 CCAACAAAGCCCTCCCWGCCCCCATCKAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 404

Qy   1118 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 1177
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Db   403 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 344

Qy   1178 GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTCGGGAGTGGGAGAGCA 1237

Db   343 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           GCCTGACCTGCCTGGTCAAAGGCTTTTATCCCAGCGACATCGCCGTGGACTCCGAGTGGGAGAGCA 284

Qy   1238 ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCT 1297
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Db   283 ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCKTCTGGACTCCGACGGCTCCT 224

Qy   1298 TCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCT 1357
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Db   223 TCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCT 164

Qy   1358 CATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCGTGT 1417
           ||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db   163 CATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCTTTT 104

Qy   1418 CTCCGGGTAAAATGA 1431
           |||||||||||||||
Db   103 CTCCGGGTAAAATGA 90

RESULT 2
BX414495/c
LOCUS   BX414495   1142 bp   mRNA   linear   EST 13-MAY-2003
DEFINITION BX414495 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001YI13
            3-PRIME, mRNA sequence.
ACCESSION   BX414495
VERSION   BX414495.1 GI:30637021
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1142)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0CAP001AE07NP1&cluster=7198.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0CAP001AE07NP1.
FEATURES   Location/Qualifiers
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             /clone_lib="Homo sapiens THYMUS"
             /note="vector: pCMVSPORT_6; 1st strand cDNA was primed
             with a NotI-oligo(dT) primer. Five prime end enriched,
             double-strand cDNA was digested with Not I and cloned into
             the Not I and EcoRV sites of the pCMVSPORT 6 vector.
             Library was not normalized."
BASE COUNT   193 a   290 c   381 g   251 t   27 others
ORIGIN

Query Match   65.0%;   Score 929.6;   DB 13;   Length 1142;
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Matches 952;   Conservative   6;   Mismatches   9;   Indels   2;   Gaps   2;

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Db   1078 TTTCCCCTTGGACCCTCCTCCAAAGAGMACTTCTCGGGGG-AMAGCSGCCCTGGGCGTGCCTG 1020

Qy   523 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC 582

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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      October  2, 2003, 13:10:05 ; Search time 76.0531 Seconds
                                          (without alignments)
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Perfect score: 1431
Sequence:    1 ATGAAACACCTGTGGTTCTT.........CCCTGTCTCCGGTAAATGA 1431

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched :   569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:        1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        score greater than or equal to the score of the result being printed,
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; Patent No. 6113898
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;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC Compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/487,550
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
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;    STRANDEDNESS: not relevant
;    TOPOLOGY: linear
;   MOLECULE TYPE: peptide
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; Patent No. 6692134
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;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
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;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/526,098
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 3:
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;   LENGTH: 1431 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide

GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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9	1315.8	91.9	1431	13	US-10-124-905-11	Sequence 11, Appl
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11	1171.4	81.9	1404	14	US-10-211-357-7	Sequence 7, Appli
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ALIGNMENTS

RESULT 1
US-09-948-429B-3
; Sequence 3, Application US/09948429B
; Patent No. US2002017769A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/948,429B
;   FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021

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;  INFORMATION FOR SEQ ID NO: 3:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 1431 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: not relevant
;    TOPOLOGY: linear
;  MOLECULE TYPE: peptide
;  FEATURE:
;    NAME/KEY: CDS
;    LOCATION: 1..1431
;  FEATURE:
;    NAME/KEY: mat.peptide
;    LOCATION: 1..1431
US-09-948-429B-3

Query Match        100.0%;  Score 1431;  DB 10;  Length 1431;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 1431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431


RESULT 2
US-10-124-807-3
; Sequence 3, Application US/10124807
; Publication No. US2003016207A1
GENERAL INFORMATION:
  APPLICANT: Anderson, Darrell R.
  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
  NUMBER OF SEQUENCES: 12
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
    STREET: 699 Prince Street
    CITY: Alexandria
    STATE: VA
    COUNTRY: USA
    ZIP: 22314
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/124,807
    FILING DATE:
    CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/383,916
    FILING DATE:
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              GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   October  2, 2003, 08:56:23 ; Search time 55.856 Seconds
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Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:      1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2577	100.0	476	18	AAW01818	Primatised anti-hu
2	2577	100.0	476	19	AAW63761	Macaque primatized
3	2577	100.0	476	23	AAU11539	Protein sequence o
4	2309	89.6	476	18	AAW01822	Primatised anti-hu
5	2309	89.6	476	19	AAW63765	Macaque primatized
6	2309	89.6	476	23	AAU11646	Protein sequence o
7	2277.5	88.4	473	22	AAB36206	Human immune syste
8	2262	87.8	470	21	AAY44721	Human immune syste
9	2230.5	86.6	475	17	AAR93553	Monoclonal antibod
10	2223	86.3	472	17	AAR93166	Anti-rhesus D reco
11	2197	85.3	453	24	ABP96295	4A5-3.1.1-B4 antib
12	2131	82.7	462	21	AAB26884	Human immunoglobul
13	2122	82.3	470	13	AAR22757	Reshaped CAMPATH-1
14	2112.5	82.0	467	13	AAW14927	Human gamma-4PE he
15	2111.5	81.9	475	18	AAW14925	Human gamma-4 heav
16	2107.5	81.8	467	22	AAG63640	Amino acid sequenc
17	2104.5	81.7	467	18	AAW14926	Human gamma-4E hea
18	2104.5	81.7	581	22	AAB81972	Ganglioside GD2 sp
19	2103.5	81.6	467	13	AAR22759	Reshaped CD4 antib
20	2100.5	81.5	467	13	AAR22758	Reshaped CD4 antib
21	2100	81.5	451	20	AAW95659	Mus musculus anti-
22	2100	81.5	451	20	AAW95661	Mus musculus anti-
23	2100	81.5	451	22	AAY85201	Light chain amino
24	2100	81.5	451	22	AAB47088	Anti-IgE antibody,
25	2100	81.5	451	22	AAB76948	Full length heavy
26	2100	81.5	451	22	AAB76950	Full length heavy
27	2095	81.3	468	23	AAE27928	Human C5E10 antibo
28	2095	81.3	468	24	ABB82837	Antibody C5E10 hea
29	2092	81.2	451	20	AAY50031	Human E27 anti-IgE
30	2092	81.2	451	20	AAW95663	Mus musculus anti-
31	2092	81.2	451	21	AAB07473	Amino acid sequenc
32	2092	81.2	451	22	AAB74212	E27 anti-IgE antib
33	2092	81.2	451	22	AAB76952	Full length heavy
34	2091.5	81.2	446	17	AAW05829	Humanised 1D10 ant
35	2084.5	80.9	472	24	ABP58289	Humanised 10D5 ant
36	2079.5	80.7	475	18	AAW11639	Human anti-RSV mon
37	2073	80.6	470	21	AAU77289	Protein #2 in inve
38	2073	80.4	478	19	AAW63763	Macaque primatized
39	2073	80.4	478	23	AAU11644	Protein sequence o
40	2069.5	80.3	481	23	AAR24442	Sequence of antibo
41	2069	80.3	453	14	AAR33311	Humanised MaEll Ve
42	2069	80.3	453	21	AAY85199	Heavy chain amino
43	2067	80.0	453	18	AAW01820	Primatised anti-hu
44	2062	80.0	470	23	AAE27923	Human C2B8 antibod
45	2062	80.0	470	24	ABB82832	Antibody C2B8 heav

ALIGNMENTS

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RESULT 1
AAW01818
ID   AAW01818 standard; Protein; 476 AA.
XX
AC   AAW01818;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US10053.
XX
PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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DR   WPI; 1997-108638/10.
DR   N-PSDB; AAT62510.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 6; Fig 8B; 81pp; English.
XX
CC   2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised
CC   forms of the light and heavy chains of cynomoigus monkey anti-human
CC   B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy
CC   variable genes (see also AAT62509 and AAT62510) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01819-22). The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence   476 AA;

Query Match          100.0%;     Score 2577;     DB 18;     Length 476;
Best Local Similarity 100.0%;     Pred. No. 1.3e-146;
Matches 476;     Conservative  0;     Mismatches  0;     Indels  0;     Gaps  0;

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Qy  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
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Qy  361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
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Qy  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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RESULT 2
AAW63761
ID   AAW63761 standard; Protein; 476 AA.
XX
AC   AAW63761;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 7C10 heavy chain DNA.
XX
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US19906.
XX
PR   08-NOV-1996;   96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,   Brams P,   Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35485.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 3b; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 7C10 heavy
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence   476 AA;

Query Match          100.0%;     Score 2577;     DB 19;     Length 476;
Best Local Similarity 100.0%;     Pred. No. 1.3e-146;
Matches 476;     Conservative  0;     Mismatches  0;     Indels  0;     Gaps  0;

Qy    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT 60
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Db    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT 60

Qy   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120

Qy  121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

Qy  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy  301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
                    GenCore version 5.1.6
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:       October   2, 2003, 09:07:34 ; Search time 20.9182 Seconds
                                            (without alignments)
                                            2188.349 Million cell updates/sec

Title:        US-09-758-173-4
Perfect score: 2577
Sequence:     1 MKHLWFFLLLVAAPRWVLSQ........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:     283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:        283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
              Maximum Match 100%
              Listing first 45 summaries

Database :    PIR_76:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1763	68.4	330	1	GHHU	Ig gamma-1 chain C
2	1626.5	63.1	377	2	A23511	Ig gamma-3 chain C
3	1624.5	63.0	377	2	A60764	Ig gamma-3 chain C
4	1600	62.1	326	1	G2HU	Ig gamma-2 chain C
5	1586.5	61.6	327	1	G4HU	Ig gamma-4 chain C
6	1537	59.6	470	2	S22080	Ig heavy chain pre
7	1525	59.2	472	2	S31459	Ig gamma-1 chain C
8	1487	57.7	374	2	S69339	Ig heavy chain V r
9	1408.5	54.7	469	2	S37483	Ig gamma-2a chain
10	1376.5	53.4	444	2	PC4436	monoclonal antibod
11	1370	53.2	446	2	S40295	Ig gamma-2a chain
12	1341	52.0	474	2	G2MS11	Ig gamma-2b chain
13	1329.5	51.6	475	2	S01321	Ig gamma-2b chain
14	1259	48.9	328	2	I47159	Ig gamma-2a chain
15	1256	48.7	255	4	S31866	Ig gamma-1 chain C
16	1253	48.6	328	2	I47160	Ig gamma-2b chain
17	1250	48.5	234	2	PT0207	Ig gamma chain C r
18	1227	47.6	328	2	I47158	Ig gamma 1 chain c
19	1226.5	47.6	323	1	GHRB	Ig gamma chain C r
20	1223	47.5	328	2	I47161	Ig gamma-3 chain c
21	1212.5	47.1	329	1	G2GP	Ig gamma-2 chain C
22	1157.5	44.9	308	2	C30554	Ig heavy chain C r
23	1152	44.7	289	1	G3HUWI	Ig gamma-3 heavy c
24	1148	44.5	326	2	PS0017	Ig gamma-1 chain C
25	1142.5	44.3	333	1	PS0018	Ig gamma-2b chain
26	1138	44.2	324	1	G1MS	Ig gamma-1 chain C
27	1137	44.1	329	1	G3MSC	Ig gamma-3 chain C
28	1133	44.0	393	1	G1MSM	Ig gamma-1 chain C
29	1126	43.7	398	1	G3MSM	Ig gamma-3 chain C
30	1122	43.5	330	1	G2MSA	Ig gamma-2a chain
31	1119.5	43.4	335	1	G2MSAB	Ig gamma-2a chain
32	1117	43.3	399	1	G2MSAM	Ig gamma-2a chain
33	1114.5	43.2	329	1	S00847	Ig gamma-2c chain
34	1108	43.0	322	2	PS0019	Ig gamma-2a chain
35	1088.5	42.2	327	2	S06611	Ig gamma-2 chain C
36	1080	41.9	405	1	G2MSBM	Ig gamma-2b chain
37	1062	41.2	277	2	I47162	Ig gamma 4 chain C
38	908	35.2	548	2	S38864	Ig epsilon chain C
39	903	35.0	220	2	A49444	Ig gamma-1 heavy c
40	794.5	30.8	549	2	S04845	Ig heavy chain pre
41	771	29.9	592	2	S25705	Ig mu chain - shee
42	727.5	28.2	572	2	B46529	Ig Y heavy chain (
43	719	27.9	627	2	S14683	Ig mu chain precur
44	713.5	27.7	249	2	S69340	Ig heavy chain VHI
45	709.5	27.5	241	2	S69131	Ig heavy chain (DO

ALIGNMENTS

```
RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1991 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:217370
A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:217370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:217370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96, R', 98-135 <CUN>
A;Note: this sequence has the Glm(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni
```

igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A:Note: this sequence has the Glm(17) and Glm(1) markers
R:Schmid, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulin IgG1 KOL
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-265,'D',268-271,'D',273-330 <SCH
A:Note: this sequence has the Glm(3) and Glm(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
A:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:243-310/Domain: immunoglobulin homology <IM3>
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
C:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:20-85/Domain: immunoglobulin homology <IM1>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match   68.4%;   Score 1763; DB 1; Length 330;
Best Local Similarity   99.7%;   Pred. No. 3.9e-97;
Matches   329;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy   267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy   327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy   387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy   447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           ||||||||||||||||||||||||||||||
Db   301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577055
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match   63.1%;   Score 1626.5; DB 2; Length 377;
Best Local Similarity   81.7%;   Pred. No. 5.2e-89;
Matches   308;   Conservative   10;   Mismatches   12;   Indels   47;   Gaps   1;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
           |||||||||||||| :|||||||||||||||||||||||||||||||||||||||||||
Db   1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA------------ 244
           |||||||||||||||||||||||||||||||||||||
Db   61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVELKTPLGDTHTCPRCPEPKSC 120

Qy   245 ------------EPKSCDKTHTCPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 279
                       ||| | |||||||||| ||||||||||||
Db   121 DTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy   280 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 339
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy   340 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 399
           |||||||||||||||||||||||||||||||||||||| :||||||||||||||||||||
Db   241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy   400 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 459
           ||||||||||||||||||||| ||||||| |||||||||||||||||||||||||||
Db   301 GFYPSDIAVEWESSGQPENNYNTTPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE 360

Qy   460 ALHNHYTQKSLSLSPGK 476
           |||| :|||||||||
Db   361 ALNNRFTQKSLSLSPGK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

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          GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:    October  2, 2003, 08:56:23 ; Search time 13.1295 Seconds
                                        (without alignments)
                                        1704.917 Million cell updates/sec

Title:       US-09-758-173-4
Perfect score: 2577
Sequence:      1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:          127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     SwissProt_41:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                          SUMMARIES
```

```
Result          Query
 No.   Score   Match  Length  DB  ID           Description
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   1   1763     68.4    330    1  GC1_HUMAN    P01857 homo sapien
   2   1600     62.1    326    1  GC2_HUMAN    P01859 homo sapien
   3   1586.5   61.6    327    1  GC4_HUMAN    P01861 homo sapien
   4   1226.5   47.6    323    1  GC_RABIT     P01870 oryctolagus
   5   1212.5   47.1    329    1  GC2_CAVPO    P01862 cavia porce
   6   1157     44.9    290    1  GC3_HUMAN    P01860 homo sapien
   7   1148     44.5    326    1  GC1_RAT      P20759 rattus norv
   8   1142.5   44.3    333    1  GCB_RAT      P20761 rattus norv
   9   1138     44.2    324    1  GC1_MOUSE    P01868 mus musculu
  10   1137     44.1    329    1  GC3_MOUSE    P22436 mus musculu
  11   1133     44.0    393    1  GC1M_MOUSE   P01869 mus musculu
  12   1126     43.7    398    1  GC3M_MOUSE   P03987 mus musculu
  13   1122     43.5    330    1  GCAA_MOUSE   P01863 mus musculu
  14   1119.5   43.4    335    1  GCAB_MOUSE   P01864 mus musculu
  15   1117     43.3    399    1  GCAM_MOUSE   P01865 mus musculu
  16   1114.5   43.2    329    1  GCC_RAT      P20762 rattus norv
  17   1108     43.0    322    1  GCB_MOUSE    P20760 rattus norv
  18   1085     42.1    336    1  GC3M_MOUSE   P01866 mus musculu
  19   1080     41.9    405    1  GCBM_MOUSE   P01867 mus musculu
  20    489     19.0    428    1  EPC_HUMAN    P01854 homo sapien
  21    483.5    18.8    429    1  EPC_RAT      P01855 rattus norv
  22    468      18.2    146    1  HV2I_HUMAN   P06331 homo sapien
  23    465      18.0    421    1  EPC_MOUSE    P06336 mus musculu
  24    442      17.2    454    1  MUC_HUMAN    P01871 homo sapien
  25    441.5    17.1    455    1  MUC_MOUSE    P01872 mus musculu
  26    437      17.1    458    1  MUC_RABIT    P03988 oryctolagus
  27    431.5    16.7    476    1  MUCM_MOUSE   P01873 mus musculu
  28    427      16.6    479    1  MUCM_RABIT   P04221 oryctolagus
  29    425      16.5    457    1  MUC_SUNMU    P20768 suncus muri
  30    420      16.3    450    1  MUC_CANFA    P01874 canis famil
  31    415.5    16.1    454    1  MUC_MESAU    P06337 mesocricetu
  32    403      15.6    391    1  MUCB_HUMAN   P04220 homo sapien
  33    394      15.3    438    1  HVCS_HETFR   P23087 heterodontu
```

```
  34    390.5    15.2    370    1  HVC1_HETFR   P23084 heterodontu
  35    386.5    15.0    438    1  HVC2_HETFR   P23085 heterodontu
  36    385      14.9    461    1  HVCM_HETFR   P23088 heterodontu
  37    383.5    14.9    353    1  ALC1_HUMAN   P01876 homo sapien
  38    380.5    14.8    353    1  ALC1_GORGO   P20758 gorilla gor
  39    379      14.7    340    1  ALC2_HUMAN   P01877 homo sapien
  40    371      14.4    129    1  HV2F_HUMAN   P01824 homo sapien
  41    362.5    14.1    393    1  HVC3_HETFR   P23086 heterodontu
  42    361      14.0    117    1  HV2G_HUMAN   P01825 homo sapien
  43    356.5    13.8    137    1  HV46_MOUSE   P01822 mus musculu
  44    355      13.8    116    1  HV60_MOUSE   P18531 mus musculu
  45    344      13.3    344    1  ALC_MOUSE    P01878 mus musculu
```

```
                                                   ALIGNMENTS

RESULT 1
GC1_HUMAN
ID   GC1_HUMAN      STANDARD;      PRT;   330 AA.
AC   P01857;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-1 chain C region.
GN   IGHG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82274238; PubMed=6287432;
RA   Ellison J.W., Berson B.J., Hood L.E.;
RT   "The nucleotide sequence of a human immunoglobulin C gammal gene.";
RL   Nucleic Acids Res. 10:4071-4079(1982).
RN   [2]
RP   SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [3]
RP   SEQUENCE OF 136-329 (EU).
RX   MEDLINE=71064025; PubMed=5530842;
RA   Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA   Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL   Biochemistry 9:3171-3181(1970).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN NIE).
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [5]
RP   SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
```

```
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002123;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
CC       G1M(1) MARKERS, 239-D & 241-L.KOL & EU SEQUENCES HAVE THE G1M(3)
CC       MARKER & THE G1M (NON-1) MARKERS.
CC   -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC       35,116,198,269 & 272.
CC   -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC       155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC       268-272.
CC   -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC       RESIDUES 198,267&272.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   ----------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GHHU.
DR   PDB; 1FC1; 15-JUL-92.
DR   PDB; 1FC2; 15-JUL-92.
DR   PDB; 1AJ7; 12-NOV-97.
DR   PDB; 1D5B; 09-FEB-00.
DR   PDB; 1D5I; 09-FEB-00.
DR   PDB; 1D6V; 04-OCT-00.
DR   PDB; 1DN2; 17-MAY-00.
DR   PDB; 1E4K; 06-JUN-01.
DR   PDB; 1FCC; 20-JUL-95.
DR   PDB; 1H2H; 12-JUN-02.
DR   PDB; 1I7Z; 08-AUG-01.
DR   PDB; 1IIS; 16-MAY-01.
DR   PDB; 1IIX; 16-MAY-01.
DR   PDB; 1L6X; 10-APR-02.
DR   PDB; 2RCS; 12-NOV-97.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100;
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    223       CH2.
```

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FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       INTERCHAIN (WITH LIGHT CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   CARBOHYD    180    180       N-LINKED (GLCNAC...).
FT   MOD_RES     330    330       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT      97     97       K -> R (IN G1M(3) MARKER).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003888.
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    147
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    166
FT   TURN        168    171
FT   STRAND      176    179
FT   TURN        180    181
FT   STRAND      182    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      260    265
FT   STRAND      270    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   STRAND      283    284
FT   TURN        287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      305    312
FT   TURN        313    314
FT   TURN        316    317
FT   STRAND      320    325
SQ   SEQUENCE    330 AA;  36106 MW;  3770EE10G62FA33D CRC64;
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Query Match             68.4%;  Score 1763;  DB 1;  Length 330;
Best Local Similarity   99.7%;  Pred. No. 2.3e-117;
Matches  329;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   0;

Qy      147  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  206
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS   60

Qy      207  GLYSLSSVVTVPSSSLGTQYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG  266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61  GLYSLSSVVTVPSSSLGTQYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG  120

Qy      267  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQYN  326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQYN  180

Qy      327  STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVTLPPSRDE  386
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVTLPPSRDE  240

Qy      387  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFLYSKLTVDKSRW  300
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OM protein - protein search, using sw model

```
                 GenCore version 5.1.6
        Copyright (c) 1993 - 2003  Compugen Ltd.
```

Run on: October 2, 2003, 08:56:23 ; Search time 46.0645 Seconds
                                        (without alignments)
                                        2666.544 Million cell updates/sec

Title: US-09-758-173-4
Perfect score: 2577
Sequence: 1 MKHLWFFLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_23:*
         1:   sp_archea:*
         2:   sp_bacteria:*
         3:   sp_fungi:*
         4:   sp_human:*
         5:   sp_invertebrate:*
         6:   sp_mammal:*
         7:   sp_mhc:*
         8:   sp_organelle:*
         9:   sp_phage:*
        10:   sp_plant:*
        11:   sp_rodent:*
        12:   sp_virus:*
        13:   sp_vertebrate:*
        14:   sp_unclassified:*
        15:   sp_rvirus:*
        16:   sp_bacteriap:*
        17:   sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2041.5	79.2	471	4	Q8TC77	Q8tc77 homo sapien
2	2017	78.3	473	4	Q8TC63	Q8tc63 homo sapien
3	1884.5	73.1	521	4	Q8N4Y9	Q8n4y9 homo sapien
4	1614	62.6	509	4	Q8NF17	Q8nf17 homo sapien
5	1429	55.5	469	11	Q8R3V9	Q8r3v9 mus musculu
6	1423.5	55.2	463	11	Q99LC4	Q99lc4 mus musculu
7	1405	54.5	468	11	Q99L31	Q99l31 mus musculu
8	1403.5	54.5	473	11	Q9DBL4	Q9dbl4 mus musculu
9	1389.5	53.9	437	11	Q9R1A4	Q9r1a4 mus musculu
10	1383.5	53.7	473	11	Q99L25	Q99l25 mus musculu
11	1333.5	51.7	473	11	Q91Z05	Q91z05 mus musculu
12	1326	51.4	474	11	Q8R3H6	Q8r3h6 mus musculu
13	1268	49.2	701	4	Q96PQ8	Q96pq8 homo sapien
14	1262.5	49.0	337	6	Q95M34	Q95m34 equus cabal
15	950.5	36.9	597	4	Q9BU10	Q9bu10 homo sapien
16	948.5	36.8	597	4	Q9BQB8	Q9bqb8 homo sapien
17	940.5	36.5	588	4	Q8WUX4	Q8wux4 homo sapien
18	940.5	36.5	618	4	Q96AA6	Q96aa6 homo sapien
19	931	36.1	613	4	Q96EY0	Q96ey0 homo sapien
20	856	33.2	496	4	Q96KX8	Q96kx8 homo sapien
21	745.5	28.9	597	4	Q96BB9	Q96bb9 homo sapien
22	727.5	28.2	479	11	Q99M22	Q99m22 mus musculu
23	719	27.9	613	11	Q8VCX7	Q8vcx7 mus musculu
24	718	27.7	613	11	Q8WUK1	Q8wuk1 homo sapien
25	712	27.6	278	11	Q921K1	Q921k1 mus musculu
26	693.5	26.9	499	4	Q8N5K4	Q8n5k4 homo sapien
27	691.5	26.8	614	4	Q96GA6	Q96ga6 homo sapien
28	688	26.7	482	11	Q91X92	Q91x92 mus musculu
29	665	25.8	494	4	Q96K68	Q96k68 homo sapien
30	654.5	25.4	493	4	Q8NCL6	Q8ncl6 homo sapien
31	651	25.3	496	4	Q96DK0	Q96dk0 homo sapien
32	640	24.8	500	4	Q9BRV0	Q9brv0 homo sapien
33	632	24.5	488	11	Q91WR1	Q91wr1 mus musculu
34	631.5	24.5	487	11	Q99KA4	Q99ka4 mus musculu
35	630.5	24.5	497	4	Q8WY24	Q8wy24 homo sapien
36	629.5	24.4	481	11	Q91WT1	Q91wt1 mus musculu
37	625	24.3	486	11	Q91Z07	Q91z07 mus musculu
38	621.5	24.1	481	11	Q8VCV5	Q8vcv5 mus musculu
39	620.5	24.1	479	11	Q91WP5	Q91wp5 mus musculu
40	618.5	24.0	484	11	Q8VEA0	Q8vea0 mus musculu
41	617.5	24.0	480	11	Q91XE1	Q91xe1 mus musculu
42	616	23.9	482	11	Q8K172	Q8k172 mus musculu
43	612	23.7	488	11	Q8K0F2	Q8k0f2 mus musculu
44	607.5	23.6	481	11	Q91WT3	Q91wt3 mus musculu
45	600.5	23.3	489	11	Q8VCX4	Q8vcx4 mus musculu

ALIGNMENTS

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RESULT 1
Q8TC77
ID   Q8TC77;       PRELIMINARY;   PRT;   471 AA.
AC   Q8TC77;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024289; AAH24289.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE 471 AA;  51791 MW;  388F7F4CF58660E CRC64;

Query Match             79.2%;  Score 2041.5;  DB 4;  Length 471;
Best Local Similarity   82.8%;  Pred. No. 1.7e-164;
Matches  391;  Conservative  22;  Mismatches  52;  Indels   7;  Gaps   4;

Qy      5 WFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQTPGRG 64
          |||   ||| ||| |  |:::| ||::| :|  | ||::| |:|  |||:|| :|||||
Db      7 WVF--LVAILEGVQCEVQLVESGGGLVKPGGSLRLSCAASGFTFSS-YSMNWVRQAPGKG 63

Qy     65 LEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPRPDC 124
          |||  ||: |  ::|  ||| ||:|  | | :||||  |:: |  | |||||| |||
Db     64 LEWVSSMSSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLR-QL 122
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Qy  125 TTICYGGWDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 184
        ||||  :|:  ||||||||||||||||||||||||||||||||||||||||||||||||
Db  123 TSYWY---FDLWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 179

Qy  185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA 244
        |||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db  180 VSWNSGALTSGVHTFPAVLQSSGLYSLSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV 239

Qy  245 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 304
        |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db  240 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 299

Qy  305 NWYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 364
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  300 NWYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 359

Qy  365 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 424
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  360 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 419

Qy  425 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  420 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
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RESULT 2
Q8TC63
ID   Q8TC63
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match   78.3%; Score 2017; DB 4; Length 473;
Best Local Similarity 81.3%; Pred. No. 2.1e-162;
Matches 388; Conservative 29; Mismatches 48; Indels 12; Gaps 4;
```

```
Qy    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSI-SGYYWTWIRQ 59
        ||||||||||||||||||:  |:::    |:|| :  |: |:|:|| : ::|||  :|
Db    8 MKHLWFFLLLVAAPRWVLSRLQQESGPGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQ 67

Qy   60 TPGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARG 119
        :||:|||||| |   :   | ||:|:||||:|   ::| | |:| ||  ||||||||: |
Db   68 PPGKGLEWIGTINFSG-NMYYSPSLRSRVTMSADMSENSFYLKLDSVTAADTAVYYCAAG 126

Qy  120 PRPDCTTICYGGWDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
             :    :|     |  | | |||| |||||||||||||| :|||| :||||||||||||
Db  127 H------LVMGFGAHWGCQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF 179

Qy  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKRPSNTK 239
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Qy  240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
        ||| :|||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db  240 VDKRVESK--YGPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQED 296

Qy  300 PEVKFNWYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
        |||:|||||||||||||||||||:|||||||||||||||||||||||||||||||:||:
Db  297 PEVQFNWYDGVEVHNAKTKPREEQFNSTYRVVSVLITVLHQDWLNGKEYKCKVSNKGLPS 356

Qy  360 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
         |||||||||||||||||||||||| :|:|||||||||||||||||||||||||||||||
Db  357 SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 416

Qy  420 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        |||||||||||||||||||:||||||||:|||||||||||||||||||||||||:||
Db  417 YKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 473
```

```
RESULT 3
Q8N4Y9
ID   Q8N4Y9
AC   Q8N4Y9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells from Tonsils;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033178; AAH33178.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match   73.1%; Score 1884.5; DB 4; Length 521;
Best Local Similarity 70.2%; Pred. No. 4e-151;
Matches 368; Conservative 32; Mismatches 61; Indels 63; Gaps 5;
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Qy    7 FLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQTPGRGLE 66
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Db    7 WVLLVFLQGVQCEVQLVDSGGGLVQPGGSLRLSCAASGFIVSDHYV-EWRQAPGKGPE 65

Qy   67 WIG--HIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCAR-----G 119
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Db   66 WVGCFRSKAHKSTTEYAASVKGRFTILRDDSKNSVHLQMNSLKTDDTAVYICVRDLEGAG 125

Qy  120 PRPDCTTICYGGWDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
                       :    : |  ||||||||||||||||||| : :||||||||||||||||
Db  126 K-------YDWYFDIWGRGILVTVSSASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYF 177

Qy  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
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Db  238 VDKRVELKTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTP 297
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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:      October  2, 2003, 09:12:09 ; Search time 21.1407 seconds
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Perfect score: 2577
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Scoring table: BLOSUM62
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Searched:    328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:        328717

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Post-processing: Minimum Match 0%
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       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the total score of the result being printed,
       and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match %	Length	DB	ID	Description
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2	2577	100.0	476	4	US-09-526-098-4	Sequence 4, Appli
3	2309	89.6	476	3	US-08-487-550-12	Sequence 12, Appl
4	2309	89.6	476	4	US-09-526-098-12	Sequence 12, Appl
5	2277.5	88.4	473	4	US-09-049-672A-4	Sequence 4, Appli
6	2206	85.6	472	3	US-08-793-450-8	Sequence 8, Appli
7	2112.5	82.0	467	3	US-08-523-894-2	Sequence 12, Appli
8	2111.5	81.9	467	4	US-08-523-894-8	Sequence 8, Appli
9	2106.5	81.7	446	3	US-08-397-411-7	Sequence 7, Appli
10	2104.5	81.7	467	2	US-08-523-894-10	Sequence 10, Appli
11	2100	81.5	451	2	US-08-887-352B-14	Sequence 14, Appli
12	2100	81.5	451	3	US-08-887-352B-16	Sequence 16, Appli
13	2100	81.5	451	3	US-08-466-151-65	Sequence 65, Appli
14	2100	81.5	451	3	US-09-109-207C-14	Sequence 14, Appli
15	2100	81.5	451	3	US-09-109-207C-16	Sequence 16, Appli
16	2100	81.5	451	3	US-09-296-005-14	Sequence 14, Appli
17	2100	81.5	451	3	US-09-296-005-16	Sequence 16, Appli
18	2092	81.2	451	2	US-08-887-352B-18	Sequence 18, Appli
19	2092	81.2	451	3	US-09-109-207C-18	Sequence 18, Appli
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21	2092	81.2	451	3	US-09-054-255-2	Sequence 2, Appli
22	2092	81.2	451	3	US-09-296-005-18	Sequence 18, Appli
23	2092	81.2	451	4	US-09-282-846-2	Sequence 2, Appli
24	2092	81.2	451	4	US-09-680-145-2	Sequence 2, Appli
25	2075.5	80.5	475	4	US-09-740-002-25	Sequence 25, Appli
26	2073	80.4	478	3	US-08-487-550-8	Sequence 8, Appli
27	2073	80.4	478	4	US-09-526-098-8	Sequence 8, Appli

28	2069	80.3	453	3	US-08-466-151-8	Sequence 8, Appli
29	2069	80.3	453	4	US-08-466-163B-8	Sequence 8, Appli
30	2061.5	80.0	452	3	US-09-027-449-71	Sequence 71, Appl
31	2061.5	80.0	452	3	US-09-026-985-71	Sequence 71, Appl
32	2061.5	80.0	452	4	US-09-121-952A-71	Sequence 71, Appl
33	2047.5	79.5	452	4	US-09-234-340A-71	Sequence 71, Appl
34	2039	79.1	475	4	US-09-740-002-27	Sequence 27, Appl
35	2039	79.1	476	2	US-08-378-939-10	Sequence 10, Appl
36	2032.5	78.9	449	4	US-09-679-397-2	Sequence 2, Appli
37	2032.5	78.9	449	4	US-09-680-148-2	Sequence 2, Appli
38	2032.5	78.9	449	4	US-09-304-465A-2	Sequence 2, Appli
39	2025	78.6	449	1	US-08-458-516-13	Sequence 13, Appl
40	2019.5	78.4	462	4	US-09-289-942A-7	Sequence 7, Appli
41	2003.5	77.7	459	1	US-08-157-101A-7	Sequence 7, Appli
42	1998	77.5	472	4	US-09-301-593-30	Sequence 30, Appli
43	1997.5	77.5	467	3	US-09-049-672A-8	Sequence 8, Appli
44	1978	76.8	472	4	US-09-301-593-43	Sequence 43, Appl
45	1976.5	76.7	453	4	US-09-301-593-18	Sequence 18, Appl

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                                   ALIGNMENTS

RESULT 1
US-08-487-550-4

; Sequence 4, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES:  12
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/487,550
;    FILING DATE: 07-JUN-1995
;    CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
;    TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO: 4:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 476 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-08-487-550-4

Query Match            100.0%;  Score 2577;  DB 3;  Length 476;
Best Local Similarity  100.0%;  Pred. No. 4.6e-206;
Matches  476;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 MKHLWFFLLLVAAPRWVLSQVKLQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
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Db     1 MKHLWFFLLLVAAPRWVLSQVKLQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
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;   MOLECULE TYPE: protein
US-09-526-098-4

Query Match        100.0%;  Score 2577;  DB 4;  Length 476;
Best Local Similarity  100.0%;  Pred. No. 4.6e-206;
Matches 476;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60

Qy   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120
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Db   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120

Qy  121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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Qy  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
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Qy  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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RESULT 3
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;  Sequence 12, Application US/08487550
;  Patent No. 6113898
;  GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314
;   COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/487,550
;    FILING DATE: 07-JUN-1995
;    CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
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Qy  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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Db  301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

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;  Sequence 4, Application US/09526098
;  Patent No. 6492134
;  GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314
;   COMPUTER READABLE FORM:
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;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/526,098
;    FILING DATE:
;    CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 09/383,916
;    FILING DATE:
;    APPLICATION NUMBER: US 08/487,550
;    FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
;    TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 476 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
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          GenCore version 5.1.6
      Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:        US-09-758-173-4
Perfect score: 2577
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Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
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2	2577	100.0	476	12	US-10-124-807-4	Sequence 4, Appli
3	2577	100.0	476	12	US-10-291-532-4	Sequence 4, Appl
4	2577	100.0	476	14	US-10-124-905-4	Sequence 4, Appli
5	2309	89.6	476	10	US-09-948-429B-12	Sequence 12, Appl
6	2309	89.6	476	12	US-10-124-807-12	Sequence 12, Appl
7	2309	89.6	476	12	US-10-291-532-12	Sequence 12, Appl
8	2309	89.6	476	14	US-10-124-905-12	Sequence 12, Appl
9	2112.5	82.0	467	15	US-10-221-357-12	Sequence 8, Appli
10	2111.5	81.9	467	15	US-10-211-357-8	Sequence 10, Appl
11	2104.5	81.7	467	15	US-10-211-357-10	Sequence 66, Appli
12	2103	81.6	451	11	US-09-925-179-66	Sequence 14, Appl
13	2100	81.5	451	9	US-09-920-171-14	Sequence 16, Appl
14	2100	81.5	451	9	US-09-920-171-16	Sequence 65, Appl
15	2100	81.5	451	11	US-09-925-179-65	

16	2100	81.5	451	12	US-10-113-996-14	Sequence 14, Appl
17	2100	81.5	451	12	US-10-113-996-16	Sequence 16, Appl
18	2099	81.5	451	11	US-09-925-179-68	Sequence 68, Appl
19	2092	81.2	451	9	US-09-920-171-18	Sequence 18, Appl
20	2092	81.2	451	12	US-10-113-996-18	Sequence 18, Appl
21	2092	81.2	451	12	US-09-292-869-2	Sequence 2, Appli
22	2092	81.2	451	12	US-09-792-938-2	Sequence 2, Appli
23	2075.5	80.5	475	9	US-09-740-002-25	Sequence 25, Appl
24	2073	80.4	478	10	US-09-948-429B-8	Sequence 8, Appli
25	2073	80.4	478	12	US-10-124-807-8	Sequence 8, Appli
26	2073	80.4	478	12	US-10-291-532-8	Sequence 8, Appli
27	2073	80.4	478	14	US-10-124-905-8	Sequence 8, Appli
28	2069	80.3	453	9	US-09-802-077-8	Sequence 8, Appli
29	2069	80.3	453	9	US-09-802-096-8	Sequence 8, Appli
30	2069	80.3	453	11	US-09-925-179-8	Sequence 8, Appli
31	2061.5	80.0	452	11	US-09-726-258-71	Sequence 71, Appl
32	2055	79.7	580	12	US-10-310-719-37	Sequence 37, Appl
33	2053.5	79.7	467	15	US-10-171-452A-41	Sequence 41, Appl
34	2053.5	79.7	467	15	US-10-171-452A-47	Sequence 47, Appl
35	2053.5	79.6	467	15	US-10-171-452A-59	Sequence 59, Appl
36	2050.5	79.6	467	15	US-10-171-452A-53	Sequence 53, Appl
37	2047.5	79.5	475	9	US-09-740-002-27	Sequence 27, Appl
38	2047	79.4	451	10	US-09-996-288-230	Sequence 230, Appl
39	2047	79.4	451	11	US-09-996-265-230	Sequence 230, Appl
40	2046	79.4	474	12	US-10-225-108A-3	Sequence 3, Appli
41	2046	79.4	474	12	US-09-848-832-3	Sequence 3, Appli
42	2045.5	79.4	450	9	US-09-796-848A-43	Sequence 43, Appl
43	2045.5	79.4	450	9	US-09-796-848-49	Sequence 49, Appl
44	2045.5	79.4	450	10	US-09-996-288-216	Sequence 216, App
45	2045.5	79.4	450	10	US-09-996-288-218	Sequence 218, App

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                         ALIGNMENTS

RESULT 1
US-09-948-429B-4
; Sequence 4, Application US/09948429B
; Patent No. US2002017689A1
; GENERAL INFORMATION:
   APPLICANT: Anderson, Darrell R.
   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
   NUMBER OF SEQUENCES: 12
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
   STREET:  699 Prince Street
   CITY:  Alexandria
   STATE:  VA
   COUNTRY:  USA
   ZIP:  22314
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER:  IBM PC Compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE:  PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  US/09/948,429B
   FILING DATE:
   CLASSIFICATION:
PRIOR APPLICATION DATA:
   APPLICATION NUMBER:     09/383,916
   FILING DATE:
   APPLICATION NUMBER: US 08/487,550
   FILING DATE:  07-JUN-1995
ATTORNEY/AGENT INFORMATION:
   NAME: Teskin, Robin L.
   REGISTRATION NUMBER:  35,030
   REFERENCE/DOCKET NUMBER:  012712-131
   TELECOMMUNICATION INFORMATION:
   TELEPHONE:  703-836-6620
```

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;  TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO: 4:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 476 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-09-948-429B-4

Query Match      100.0%;    Score 2577;   DB 10;   Length 476;
Best Local Similarity   100.0%;   Pred. No. 4.8e-179;
Matches 476;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    1  MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT   60
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Db    1  MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT   60
Qy   61  PGRGLEWIGHIYGNGATNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  PGRGLEWIGHIYGNGATNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP  120
Qy  121  RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
Qy  181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
Qy  241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300
Qy  301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360
Qy  361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420
Qy  421  KTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  KTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476

RESULT 2
US-10-124-807-4
;  Sequence 4, Application US/10124807
;  Publication No. US20030166207A1
;  GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;  STREET: 699 Prince Street
;  CITY: Alexandria
;  STATE: VA
;  COUNTRY: USA
;  ZIP: 22314
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/10/124,807
;  FILING DATE:
;  CLASSIFICATION:
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;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 09/383,916
;  FILING DATE:
;  APPLICATION NUMBER: US 08/487,550
;  FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Teskin, Robin L.
;  REGISTRATION NUMBER: 35,030
;  REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 703-836-6620
;  TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO: 4:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 476 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-10-124-807-4

Query Match      100.0%;    Score 2577;   DB 12;   Length 476;
Best Local Similarity   100.0%;   Pred. No. 4.8e-179;
Matches 476;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    1  MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT   60
Qy   61  PGRGLEWIGHIYGNGATNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  PGRGLEWIGHIYGNGATNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP  120
Qy  121  RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
Qy  181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
Qy  241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300
Qy  301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360
Qy  361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420
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Db  361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420
Qy  421  KTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
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Db  421  KTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476

RESULT 3
US-10-291-532-4
;  Sequence 4, Application US/10291532
;  Publication No. US20030180290A1
;  GENERAL INFORMATION:
;  APPLICANT: HARIHARAN, KANDASAMY
;  APPLICANT: HANNA, NABIL
;  TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
;  TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
;  TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
;  FILE REFERENCE: 037003/291872
;  CURRENT APPLICATION NUMBER: US/10/291,532
;  CURRENT FILING DATE: 2002-11-12
;  PRIOR APPLICATION NUMBER: 60/331,187
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 09/758,173
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OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2003 Compugen Ltd.
GenCore version 5.1.6

Run on: October 2, 2003, 13:01:50 ; Search time 1891.24 Seconds
(without alignments)
15574.362 Million cell updates/sec

Title: US-09-758-173-5
Perfect score: 720
Sequence: 1 ATGAGGCTCCTGCTCAGCT.........TCAACAGGGGAGAGTGTTGA 720

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result. No.	Score	% Query Match	Length	DB	ID	Description
1	720	100.0	720	6	AR108864	AR108864 Sequence
2	720	100.0	720	6	AR265198	AR265198 Sequence
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4	628.4	87.3	973	9	BC022362	BC022362 Homo sapi
5	622	86.4	720	6	E40698	E40698 Antihuman F
6	620.4	86.2	891	6	E40748	E40748 Antihuman F
7	618.8	85.9	720	6	E40696	E40696 Antihuman F
8	617.2	85.7	720	6	E40697	E40697 Antihuman F
9	607.6	84.4	720	6	E40695	E40695 Antihuman F
10	506	84.2	972	9	BC030814	BC030814 Homo sapi
11	601.2	84.2	1081	6	AX540421	AX540421 Sequence
12	599.6	83.5	963	6	AX067347	AX067347 Sequence
13	599.4	83.3	830	9	AB064106	AB064106 Homo sapi
14	599.4	83.2	720	6	E35205	E35205 Human monoc
15	598.8	83.2	720	6	E35207	E35207 Human monoc
16	598.2	83.2	720	6	E35208	E35208 Human monoc
17	598	83.1	720	6	E35204	E35204 Human monoc
18	596.6	83.1	830	9	AB064102	AB064102 Homo sapi
19	595.4	82.9	720	6	E35201	E35201 Human monoc
20	593.4	82.7	720	6	E35206	E35206 Human monoc
21	591.6	82.4	720	6	E35203	E35203 Human monoc
22	591.4	82.2	720	6	E35202	E35202 Human monoc
23	588.4	82.1	977	9	BC034142	BC034142 Homo sapi
24	588.4	81.7	944	9	AK096938	AK096938 Homo sapi
25	587.8	81.7	968	6	AX616323	AX616323 Sequence
26	587.8	81.6	720	6	E35209	E35209 Human monoc
27	583.4	81.6	720	9	E35210	E35210 Human monoc
28	580.4	81.0	786	9	AB064059	AB064059 Homo sapi
29	578.8	80.6	794	9	AB064137	AB064137 Homo sapi
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31	572.4	80.4	829	9	AB064101	AB064101 Homo sapi
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33	569.2	79.3	786	9	AB064057	AB064057 Homo sapi
34	566	79.1	794	9	AB064136	AB064136 Homo sapi
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40	556.4	77.3	785	9	AB064055	AB064055 Homo sapi
41	556.4	77.3	784	9	AB064058	AB064058 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS   AR108864   720 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION   Sequence 5 from patent US 6113898.
ACCESSION   AR108864
VERSION   AR108864.1   GI:12825140
KEYWORDS   Unknown.
SOURCE   Unknown.
ORGANISM   Unclassified.
             1 (bases 1 to 720)
REFERENCE   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
AUTHORS   Human B7.1-specific primatized antibodies and transfectomas
TITLE   expressing said antibodies
JOURNAL   Patent: US 6113898-A 5 05-SEP-2000;

Pred. No. is the number of results predicted by chance to have a

FEATURES   Location/Qualifiers
source   1 ..720
                  /organism="unknown"
BASE COUNT   178 a   200 c   193 g   149 t
ORIGIN

Query Match   100.0%;   Score 720;   DB 6;   Length 720;
Best Local Similarity 100.0%;   Pred. No. 1.6e-194;
Matches 720;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db    1 ATGAGCCCTCCTGCTCAGCTCCTCGGGCGTGCTATTGCTCTGCGTCCCGGGTCCCAGTGGG 60

Qy   61 GAAGTTGTGATGACTCAGTCTCCATCACCTGGAGAGCCGGCCTCC 120
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Qy  121 ATCTCCTGTAGGGTCTAGTCAAAGCCTTAAACACAGTAATGAGACACCTTCCTGAGTTGG 180
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Db  121 ATCTCCTGTAGGGTCTAGTCAAAGCCTTAAACACAGTAATGAGACACCTTCCTGAGTTGG 180

Qy  181 TATCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240
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Db  181 TATCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240

Qy  241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGCAGGCAGGGACAGATTCACACTGAAAATC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGCAGGCAGGGACAGATTCACACTGAAAATC 300

Qy  301 AGGCCAGTGGAGGCTGAAGATGTTGGGGTTTATTCTGCGGGCAAGGTACAAGGACTCCT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AGGCCAGTGGAGGCTGAAGATGTTGGGGTTTATTCTGCGGGCAAGGTACAAGGACTCCT 360

Qy  361 CCCACTTTCGGGCGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCCACCATCTGTC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CCCACTTTCGGGCGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCCACCATCTGTC 420

Qy  421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 480
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Db  421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 480

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Db  541 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600

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Qy  661 GTCACCCATCAGGGCCTGAGCCTGCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTGA 720
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RESULT 3
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LOCUS   BD063036   720 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION   Identification of unique binding interactions between certain
              antibodies and the human B7.1 and B7.2 co-stimulatory antigens.
ACCESSION   BD063036
VERSION   BD063036.1   GI:22608639
KEYWORDS   JP 2001504693-A/3.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 720).
  AUTHORS   Anderson,D.R., Hanna,N., Brams,P. and Hard,C.

FEATURES   Location/Qualifiers
source   1 ..720
                  /organism="unknown"
BASE COUNT   178 a   200 c   193 g   149 t
ORIGIN

Query Match   100.0%;   Score 720;   DB 6;   Length 720;
Best Local Similarity 100.0%;   Pred. No. 1.6e-194;
Matches 720;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db    1 ATGAGCCCTCCTGCTCAGCTCCTCGGGCGTGCTATTGCTCTGCGTCCCGGGTCCCAGTGGG 60

Qy   61 GAAGTTGTGATGACTCAGTCTCCATCACCTGGAGAGCCGGCCTCC 120
        ||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GAAGTTGTGATGACTCAGTCTCCATCACCTGGAGAGCCGGCCTCC 120

Qy  121 ATCTCCTGTAGGGTCTAGTCAAAGCCTTAAACACAGTAATGAGACACCTTCCTGAGTTGG 180
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Db  121 ATTTCCTGTAGGGTCTAGTCAAAGCCTTAAACACAGTAATGAGACACCTTCCTGAGTTGG 180

Qy  181 TATCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TATCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240

Qy  241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGCAGGCAGGGACAGATTCACACTGAAAATC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGCAGGCAGGGACAGATTCACACTGAAAATC 300

Qy  301 AGGCCAGTGGAGGCTGAAGATGTTGGGGTTTATTCTGCGGGCAAGGTACAAGGACTCCT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AGGCCAGTGGAGGCTGAAGATGTTGGGGTTTATTCTGCGGGCAAGGTACAAGGACTCCT 360

Qy  361 CCCACTTTCGGGCGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCCACCATCTGTC 420
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Db  361 CCCACTTTCGGGCGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCCACCATCTGTC 420

Qy  421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 480

Qy  481 CTGAATAACTTCATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 CTGAATAACTTCATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 540

Qy  541 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600

Qy  601 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAAGTCTACGCCTCGCAA 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAAGTCTACGCCTGCGAA 660

Qy  661 GTCACCCATCAGGGCCTGAGCCTGCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTGA 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 GTCACCCATCAGGGCCTGAGCCTGCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTGA 720
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RESULT 2
AR265198
LOCUS   AR265198   720 bp   DNA   linear   PAT 10-APR-2003
DEFINITION   Sequence 5 from patent US 6492134.
ACCESSION   AR265198
VERSION   AR265198.1   GI:29693619
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 720).
  AUTHORS   Aquin,S. and Vezina,Louis.-P.
  TITLE   Method for producing polyhydroxyalkanoates in recombinant organisms
  JOURNAL   Patent: US 6492134-A 5 10-DEC-2002;

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                    GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:        October  2, 2003, 12:12:30  ; Search time 147.469 Seconds
                                          (without alignments)
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Title:         US-09-758-173-5
Perfect score: 720
Sequence:      1 ATGAGCTCCCTGCTCAGCT........TCAACAGGGGAGAGTGTTGA 720

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:      5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	720	100.0	720	19	AAV35486	Macaque primatized
2	720	100.0	720	24	AAS17244	DNA sequence of a
3	718.4	99.8	720	18	AAT62511	Primatised anti-hu
4	622	86.4	720	19	AAV61362	Anti-human Fas hum
5	622	86.4	720	21	AAA78270	Anti-human Fas imm
6	620.4	86.2	891	19	AAV66632	Human immunoglobul
7	620.4	86.2	891	21	AAA78320	Anti-human Fas Ig
8	618.8	85.9	720	19	AAV61360	Anti-human Fas hum

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12   617.2  85.7   720  19  AAV61359  Anti-human Fas hum
13   617.2  85.7   720  21  AAA78267  Anti-human Fas imm
14    606   84.2  1081  24  ABS51811  Human mdt cDNA In
15    601.2  83.5   963  22  AAF44895  Human breast cance
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19    598.2  83.1   720  21  AAA13923  Human PTHrP monocl
20    596.6  82.9   720  21  AAA13920  Human PTHrP monocl
21    595.4  82.7   720  21  AAA13925  Human PTHrP monocl
22    593.4  82.4   720  21  AAA13922  Human PTHrP monocl
23    591.6  82.2   720  21  AAA13921  Human PTHrP monocl
24    588.4  81.7   968  25  ACC51063  Human CalX protein
25    587.8  81.6   720  21  AAA13928  Human PTHrP monocl
26    587.8  81.6   720  21  AAA13929  Human PTHrP monocl
27    582.2  80.9   772  20  AAZ24418  Human bladder tumo
28    566.4  78.7   648  25  ABZ22307  S. pneumoniae PPS-
29    563.2  78.2   714  25  ABZ26638  Humanised 1D5 ant
30    561.2  77.9   726  17  AAT18060  Monoclonal antibod
31     558   77.5   720  21  ABK10999  DNA encoding prote
32    554.6  77.0   717  18  AAT62934  Murine anti-porcin
33    554.6  77.0  5300  25  AAT62938  3F4 human IgG4 exp
34    553.8  76.9   717  25  ABZ24632  Humanised 3D6 anti
35    551.6  76.6   925  21  AAA27395  Human TGFAM-15 imm
36    549.2  76.3   740  22  AAF63373  Humanised 323/A3 (
37    549.2  76.3   740  22  AAF63377  Anti-Ep-CAM antibo
38     541   75.1   649  25  ABZ22313  S. pneumoniae PPS-
39     533   74.0   663  22  AAD20744  Human recombinant
40     533   74.0   663  25  ABX79099  Mucin 1 (MUC-1) bi
41    527.6  73.3   737  13  AAQ25691  Sequence of the ch
42    520.6  72.3   799  24  AAD32341  Human lung specifi
43    519.2  72.1   727  21  AAZ87965  Chimeric 6G4.2.5 a
44    519.2  72.1   729  16  AAT03380  Anti-IL-8 chimeric
45    519.2  72.1   729  18  AAV03226  Murine variable re
```

ALIGNMENTS

```
RESULT 1
AAV35486
  ID   AAV35486 standard; DNA; 720 BP.
  XX
  AC   AAV35486;
  XX
  DT   29-SEP-1998  (first entry)
  XX
  DE   Macaque primatized 7B6 light chain DNA.
  XX
  KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
  KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
  KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
  KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
  KW   T cell proliferation; ss.
  XX
  OS   Macaca fascicularis.
  XX
  FH   Key             Location/Qualifiers
  FT
  FT   CDS             1..720
  FT                   /*tag= a
  FT                   /product= 7B6 light chain
  XX
  PN   WO9819706-A1.
  XX
  PD   14-MAY-1998.
  XX
  PF   29-OCT-1997;  97WO-US19906.
  XX
  PR   08-NOV-1996;  96US-0746351.
  XX
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PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63762.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 4a; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 7B6 light chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other;

Query Match   100.0%; Score 720; DB 19; Length 720;
Best Local Similarity 100.0%; Pred. No. 2.9e-182;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 GAAGTTGTGATGACTCAGTCTCCACTCTCCTTCCCATCCACACCTGGAGAGCCGGCCTCC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 121 ATCTCCTGTAGGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG 180
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Qy 181 TATCAGCAGAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240
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Qy 241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGCAGGGCAGATTCACACTGAAAATC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGCAGGGCAGATTCACACTGAAAATC 300

Qy 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360

Qy 361 CCCACTTCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 CCCACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC 420

Qy 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAAAATCTGGAACTGCCTCTGTTGTGTGCCTG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAAAATCTGGAACTGCCTCTGTTGTGTGCCTG 480

Qy 481 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 540

Qy 541 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACAGCACCTACAGCCTC 600
        |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db 541 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACAGCACCTACAGCCTC 600

Qy 601 AGCAGCACCTGACCGCTGAGCAAGCAGACTACCAGAAACACAAAGTCTACGCCTGCGAA 660
        ||||||||| |||| |||||||||||||||||| |||||||||||||||||||||||||||
Db 601 AGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 660

Qy 661 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGGAGAGTGTTGA 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db 661 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGGAGAGTGTGA 720

RESULT 2
AAS17244
ID   AAS17244 standard; DNA; 720 BP.
XX
AC   AAS17244;
XX
DT   12-MAR-2002 (first entry)
XX
DE   DNA sequence of a primatised form of the light chain of 7B6 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin 2; IL-2; mutant; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
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FT   /product= "Light chain of 7B6 antibody"
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   P-PSDB; AAU11540.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells.
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy
XX
PS   Example 8; Fig 4a; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression

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          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:05:20 ; Search time 1190.71 Seconds
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                Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215223 8056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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    29: gb_gss2:*

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7	594.4	82.6	898	13	BQ708918	BQ708918 603617168
8	592.4	82.3	726	12	BM007723	BM007723 AGENCOURT
9	592	82.2	796	14	CB956719	CB956719 AGENCOURT
10	591.8	82.2	995	13	BQ712430	BQ712430 AGENCOURT
11	590.8	82.1	952	10	BG758592	BG758592 602712820
12	587.2	81.6	720	12	BI768966	BI768966 603058111
13	587	81.5	785	14	CB958366	CB958366 AGENCOURT
14	585.8	81.4	734	14	CB984409	CB984409 AGENCOURT
15	578.4	80.3	908	10	BG685179	BG685179 602637065
16	578	80.3	859	10	BG758795	BG758795 602713155
17	576.6	80.1	771	14	CB956254	CB956254 AGENCOURT
18	574	79.7	731	14	CB985070	CB985070 AGENCOURT
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22	567.4	78.8	701	10	BG547597	BG547597 602575437
23	565.8	78.6	738	10	BG740066	BG740066 602631139
24	564.6	78.4	730	12	BI837183	BI837183 603089959
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29	555.6	77.2	875	12	BI518518	BI518518 603061638
30	554.8	77.1	907	13	BQ708655	BQ708655 AGENCOURT
31	553.6	76.9	710	12	BI908471	BI908471 603069231
32	551.6	76.6	743	14	CB957685	CB957685 AGENCOURT
33	549.6	76.3	931	10	BG757255	BG757255 602715238
34	549.2	76.3	811	14	CB956301	CB956301 AGENCOURT
35	547.4	76.0	687	14	CB552296	CB552296 MMSP0044_
36	547.4	76.0	696	12	BI838136	BI838136 603083638
37	544.2	75.6	970	12	BX437518	BX437518 BX437518
38	542.4	75.3	912	12	BI908319	BI908319 603066141
39	542	75.3	912	10	BF974515	BF974515 602243421
40	540.8	75.1	693	14	CB956992	CB956992 AGENCOURT
41	540.4	75.1	760	14	CB986353	CB986353 AGENCOURT
42	540.2	75.0	817	14	CB957285	CB957285 AGENCOURT
43	538.8	74.8	653	9	AW404795	AW404795 UI-HF-BL0
44	538.4	74.8	1009	13	BU146853	BU146853 AGENCOURT
c 45	538.2	74.8	925	13	BX437517	BX437517 BX437517

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by.analysis of the total score distribution.

                         SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	618.8	85.9	816	12	BI759427	BI759427 603043095
2	610.6	84.8	774	12	BM007808	BM007808 603611276
3	608	84.4	795	14	CB958667	CB958667 AGENCOURT
4	598.2	83.1	857	12	BI758820	BI758820 603042739

                         ALIGNMENTS

RESULT 1
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LOCUS   BI759427   816 bp   mRNA   linear   EST 25-SEP-2001
DEFINITION 603043095F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183446 5'',
            mRNA sequence.
ACCESSION   BI759427
VERSION   BI759427.1 GI:15751005
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 816)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs.r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11457 row: n column: 23
            High quality sequence start: 2

FEATURES
     source

High quality sequence stop: 814.
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               /clone_lib="NIH_MGC_116"
               /note="Organ: pooled colon, kidney, stomach; Vector:
               pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
               source anonymous pool of 3 colons, age 26 yo male, 49 yo
               female, 71 yo male colon; 46 yo male kidney, and pool of 2
               stomachs, 62 yo male and 70 yo female. Library is
               oligo-dT primed and directionally cloned (EcoRV site is
               destroyed upon cloning). Average insert size 1.4 kb,
               insert size range 1-3 kb. Library is normalized and
               enriched for full-length clones and was constructed by C.
               Gruber (Invitrogen). Research Genetics tracking code
               023. Note: this is a NIH_MGC Library."

BASE COUNT   194 a   238 c   208 g   176 t
ORIGIN

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Qy   61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCATCACACCTGGAGAGCCGGCCTCC 120
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Qy 181 TATCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTTATTAAGGTTCTAACCGGGAC 240
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Qy 361 CCCACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCGTC 420
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RESULT 2
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LOCUS   BM007808   774 bp   mRNA   linear   EST 30-OCT-2001
DEFINITION   6036I7276F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440962 5',
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ACCESSION   BM007808
VERSION   BM007808.1   GI:16522162
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 774)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov.
             Plate: LLCM1914 row: h column: 19
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                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
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                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(C). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

BASE COUNT   187 a   224 c   203 g   160 t
ORIGIN

Query Match   84.8%;   Score 610.6;   DB 12;   Length 774;
Best Local Similarity   91.6%;   Pred. No. 1.7e-160;
Matches 657;   Conservative   0;   Mismatches 59;   Indels   1;   Gaps   1;

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Qy 241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGTCAGCGGCAGTGGGTCAGCGACACTGAAAATC 300
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Fri Oct   3 08:46:39 2003

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OM nucleic - nucleic search, using sw model

Run on:    October  2, 2003, 13:10:05 ; Search time 38.2657 Seconds
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Scoring table: IDENTITY_NUC
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Searched:      569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:    1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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2	720	100.0	720	4		US-09-526-098-5	Sequence 55, Appli
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8	519.2	72.1	729	3		US-09-027-449-41	Sequence 41, Appl
9	519.2	72.1	729	3		US-08-804-444A-41	Sequence 41, Appl
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25	468.8	65.1	705	2		US-08-634-400-16	Sequence 16, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 5, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
  APPLICANT:   Anderson, Darrell R.
  TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
  TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
  TITLE OF INVENTION:  PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
  TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
  NUMBER OF SEQUENCES:  12
  CORRESPONDENCE ADDRESS:
   ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
   STREET:  699 Prince Street
   CITY:  Alexandria
   STATE:  VA
   COUNTRY:  USA
   ZIP:  22314
  COMPUTER READABLE FORM:
   MEDIUM TYPE:  Floppy disk
   COMPUTER:  IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  US/08/487,550
   FILING DATE:  07-JUN-1995
   CLASSIFICATION:  435
  ATTORNEY/AGENT INFORMATION:
   NAME:  Teskin, Robin L.
   REGISTRATION NUMBER:  35,030
   REFERENCE/DOCKET NUMBER:  012712-131
  TELECOMMUNICATION INFORMATION:
   TELEPHONE:  703-836-6620
   TELEFAX:  703-836-2021
  INFORMATION FOR SEQ ID NO:  5:
   SEQUENCE CHARACTERISTICS:
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      FILING DATE:
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      APPLICATION NUMBER: US 08/487,550
      FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
      NAME: Teskin, Robin L.
      REGISTRATION NUMBER: 35,030
      REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
      TELEPHONE: 703-836-6620
      TELEFAX: 703-836-2021
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US-09-526-098-5

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RESULT 2
US-09-526-098-5
; Sequence 5, Application US/0952609B
; Patent No. 6492134
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;     STREET: 699 Prince Street
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22314
;   COMPUTER READABLE FORM:
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;     COMPUTER: IBM compatible
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          GenCore version 5.1.6
     Copyright (c) 1993 - 2003 Compugen Ltd.

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      6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
      7: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
      8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
      9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
     10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
     11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
     12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
     13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
     14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
     15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
     16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
     17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	720	100.0	720	10	US-09-948-429B-5	Sequence 5, Appli
2	720	100.0	720	12	US-10-124-807-5	Sequence 5, Appli
3	720	100.0	720	12	US-10-291-532-5	Sequence 5, Appli
4	720	100.0	720	13	US-10-124-905-5	Sequence 3, Appli
5	720	100.0	720	13	US-10-073-138-3	Sequence 63, Appli
6	607.4	84.4	2272	14	US-10-158-646-63	Sequence 63, Appli
7	588.4	81.7	968	11	US-09-992-600A-7	Sequence 7, Appli
8	588.4	81.7	968	12	US-09-924-340-7	Sequence 7, Appli
9	588.4	81.7	968	12	US-09-992-095B-7	Sequence 7, Appli
10	588.4	81.7	968	12	US-10-154-678-7	Sequence 7, Appli
11	588.4	81.7	968	12	US-09-999-570-7	Sequence 7, Appli
12	588.4	81.7	968	14	US-10-000-489-7	Sequence 7, Appli
13	588.4	81.7	968	14	US-10-000-986-7	Sequence 7, Appli
14	585.2	81.3	738	14	US-10-158-646-91	Sequence 61, Appli
15	557.8	77.5	657	11	US-09-972-656-91	Sequence 91, Appl
16	546.6	75.9	657	11	US-09-972-656-103	Sequence 103, App
17	535.4	74.4	657	11	US-09-972-656-105	Sequence 105, App
18	533.8	74.1	657	11	US-09-972-656-93	Sequence 93, Appl
19	533	74.0	663	10	US-09-822-698A-25	Sequence 25, Appl
20	520.6	72.3	799	11	US-09-909-567B-14	Sequence 14, Appl
21	519.2	72.1	729	11	US-09-726-258-41	Sequence 41, Appl
22	504	70.0	1775	14	US-10-158-646-64	Sequence 64, Appl
23	500	69.4	717	14	US-10-171-452A-37	Sequence 37, Appl
24	500	69.4	717	14	US-10-171-452A-55	Sequence 55, Appl
25	498.4	69.2	717	14	US-10-171-452A-43	Sequence 43, Appl
26	498.4	69.2	717	14	US-10-171-452A-49	Sequence 49, Appl
27	497	69.0	1033	9	US-09-799-514-2	Sequence 2, Appli
28	494	68.6	928	14	US-10-221-945-5	Sequence 5, Appli
29	488.8	67.9	708	14	US-10-158-382-6	Sequence 6, Appli
30	487.4	67.7	788	14	US-10-158-646-58	Sequence 58, Appl
31	486	67.5	705	14	US-10-153-382-14	Sequence 14, Appl
32	484	67.2	768	12	US-10-384-933-106	Sequence 106, App
33	484	67.2	768	14	US-10-384-933-108	Sequence 108, App
34	484	67.2	768	14	US-10-216-484-106	Sequence 106, App
35	484	67.2	768	14	US-10-216-484-108	Sequence 108, App
36	483.6	67.0	702	14	US-10-150-475A-5	Sequence 5, Appli
37	482.4	67.0	768	12	US-10-384-933-51	Sequence 51, Appl
38	482.4	67.0	768	12	US-10-384-933-53	Sequence 53, Appl
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41	480.8	66.8	768	14	US-10-384-933-49	Sequence 49, Appl
42	480.8	66.8	768	14	US-10-216-484-49	Sequence 49, Appl
43	480	66.7	702	14	US-10-153-382-10	Sequence 10, Appl
44	479.4	66.6	1775	14	US-10-158-646-64	Sequence 64, Appl
45	479.2	66.6	913	10	US-09-822-830A-531	Sequence 531, App

ALIGNMENTS

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RESULT 1
US-09-948-429B-5
; Sequence 5, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;     STREET: 699 Prince Street
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22314
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/948,429B
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/383,916
;     FILING DATE:
;     APPLICATION NUMBER: US 08/487,550
;     FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Teskin, Robin L.
;     REGISTRATION NUMBER: 35,030
;     REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-836-6620
;     TELEFAX: 703-836-2021
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;  APPLICANT:  Anderson, Darrell R.
;  TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION:  PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES:  12
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;  STREET:  699 Prince Street
;  CITY:  Alexandria
;  STATE:  VA
;  COUNTRY:  USA
;  ZIP:  22314
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE:  Floppy disk
;  COMPUTER:  IBM PC compatible
;  OPERATING SYSTEM:  PC-DOS/MS-DOS
;  SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER:  US/10/124,807
;  FILING DATE:
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  09/383,916
;  FILING DATE:
;  APPLICATION NUMBER:  US 08/487,550
;  FILING DATE:  07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME:  Teskin, Robin L.
;  REGISTRATION NUMBER:  35,030
;  REFERENCE/DOCKET NUMBER:  012712-131
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE:  703-836-6620
;  TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  5:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH:  720 base pairs
;  TYPE:  nucleic acid
;  STRANDEDNESS:  not relevant
;  TOPOLOGY:  linear
;  MOLECULE TYPE:  peptide
;  FEATURE:
;  NAME/KEY:  CDS
;  LOCATION:  1..720
;  FEATURE:
;  NAME/KEY:  mat_peptide
;  LOCATION:  1..720
US-10-124-807-5
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Qy     121  ATCTCCTGTAGGTCAGTCAAAGCCTTAAACACAGTAATGGAGCACCTTCCTGAGTTGG  180
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Db     121  ATCTCCTGTAGGTCAGTCAAAGCCTTAAACACAGTAATGGAGCACCTTCCTGAGTTGG  180

Qy     181  TATCAGCAGAAGCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC  240
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Db     181  TATCAGCAGAAGCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC  240

Qy     241  TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGGACAGATTTCACACTGAAAATC  300
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Db     241  TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGGACAGATTTCACACTGAAAATC  300
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          GenCore version 5.1.6
      Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  2, 2003, 08:55:23 ; Search time 28.0453 Seconds
                                        (without alignments)
                             1352.654 Million cell updates/sec

Title:          US-09-758-173-6
Perfect score:  1242
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Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:        1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB ID	Description
1	1242	100.0	239	18	AAW01819	Primatised anti-hu
2	1242	100.0	239	19	AAW63762	Macaque primatized
3	1242	100.0	239	23	AAU11540	Protein sequence o
4	1116	89.9	239	19	AAW71879	Anti-human Fas hum
5	1116	89.9	239	21	AAB12916	Anti-human Fas imm
6	1113	89.6	239	19	AAW71877	Anti-human Fas hum
7	1113	89.6	239	19	AAW71878	Anti-human Fas hum
8	1113	89.6	239	21	AAB12914	Anti-human Fas imm
9	1113	89.6	239	21	AAB12915	Anti-human Fas imm

10	1110	89.4	239	19	AAW71876	Anti-human Fas hum
11	1110	89.4	239	21	AAB12913	Anti-human Fas imm
12	1083	87.2	239	21	AAY82615	Human PTHrP monocl
13	1081	87.0	247	23	ABG70038	Human MDDT protein
14	1070.5	86.2	238	24	ABP58288	Humanised 10D5 ant
15	1068	86.0	239	24	ABP48456	Human CalX protein
16	1065	85.7	239	21	AAY82611	Human PTHrP monocl
17	1063	85.6	239	21	AAY82610	Human PTHrP monocl
18	1063	85.6	239	21	AAY82617	Human PTHrP monocl
19	1061	85.4	239	21	AAY82614	Human PTHrP monocl
20	1057	85.1	239	21	AAY82616	Human PTHrP monocl
21	1052.5	84.7	238	18	AAW14942	3F4 Human IgG4 exp
22	1052.5	84.7	238	18	AAW14937	Murine anti-porcin
23	1050	84.5	239	21	AAY82613	Human PTHrP monocl
24	1044	84.1	239	21	AAY82612	Human PTHrP monocl
25	1042	83.9	241	21	AAY96303	Human IGFAM-15 imm
26	1041	83.8	238	24	ABP58274	Humanised 3D6 anti
27	1038.5	83.6	238	22	AAU07744	Humanised monoclon
28	1037.5	83.5	238	17	AAR93554	Monoclonal antibod
29	1033	83.2	219	24	ABP58286	Humanised 10D5 ant
30	1022	82.3	239	21	AAU77288	Protein #1 in inve
31	1018	82.0	239	21	AAY82618	Human PTHrP monocl
32	1016	81.8	239	21	AAY82619	Human PTHrP monocl
33	1009	81.2	219	24	ABB80108	Light chain. Homo
34	1009	81.2	219	24	ABR39464	Humanised anti-Abe
35	1009	81.2	219	24	ABU08310	Humanised 266 anti
36	1007	81.1	238	22	AAB72227	Humanised 323/A3 (
37	1007	81.1	238	22	AAB72231	Humanised 323/A3 (
38	1007	81.1	238	22	AAB72233	Humanised 323/A3 (
39	1007	81.1	238	22	AAB72235	Humanised 323/A3 (
40	1004	80.8	219	24	ABP58272	Humanised 3D6 anti
41	992.5	79.9	220	22	AAE12714	Human recombinant
42	992.5	79.9	220	24	ABU58806	Mucin 1 (MUC-1) b1
43	978	78.7	241	13	AAR28809	Vector pMDRI007.
44	976.5	78.6	238	19	AAW83034	Anti-Fas humanised
45	976.5	78.6	238	21	AAB14777	Humanised anti-Fas

ALIGNMENTS

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RESULT 1
AAW01819
ID   AAW01819 standard; Protein; 239 AA.
XX
AC   AAW01819;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7B6 light chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7B6;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type l diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US10053.
XX
PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
XX
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DR   WPI; 1997-108638/10.
DR   N-PSDB; AAT62511.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 8; Fig 9A; 81pp; English.
XX
CC   2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 7B6. Cloned 7B6 light and heavy
CC   variable genes (see also AAT62511 and AAT13847) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-19 and
CC   AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway,
CC   making them useful immunosuppressants for the treatment of
CC   autoimmune disorders and graft-versus-host disease.
XX
SQ   Sequence 239 AA;

Query Match   100.0%; Score 1242; DB 18; Length 239;
Best Local Similarity   100.0%; Pred. No.1.8e-69;
Matches 239; Conservative   0; Mismatches 0; Indels   0; Gaps   0;

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Db   1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60

Qy   61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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Db   61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120

Qy   121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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Db   121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180

Qy   181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 2
AAW63762
ID   AAW63762 standard; Protein; 239 AA.
XX
AC   AAW63762;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 7B6 light chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997; 97WO-US19906.
XX
PR   08-NOV-1996; 96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX

DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35486.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 4a; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 7B6 light
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   i diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 239 AA;

Query Match   100.0%; Score 1242; DB 19; Length 239;
Best Local Similarity   100.0%; Pred. No.1.8e-69;
Matches 239; Conservative   0; Mismatches 0; Indels   0; Gaps   0;

Qy   1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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Db   1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60

Qy   61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120

Qy   121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180

Qy   181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 3
AAU11540
ID   AAU11540 standard; Protein; 239 AA.
XX
AC   AAU11540;
XX
DT   12-MAR-2002 (first entry)
XX
DE   Protein sequence of primatised form of the light chain of 7B6 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; mutein.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX

```
                  GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      October  2, 2003, 09:07:34 ; Search time 10.503 Seconds
                                           (without alignments)
                                           2188.349 Million cell updates/sec

Title:           US-09-758-173-6
Perfect score:   1242
Sequence:        1 MSLPAQLLGLLLLCVPGSSG.........EVTHQGLSSPVTKSFNRGEC 239

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:        283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_76:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                           SUMMARIES
```

```
Result          %
No.   Score  Query  Match Length DB  ID      Description
             Match
---   -----  -----  ----- ------ --  ------   -----------
  1     915   73.7         215    2  JE0244   Ig kappa chain NIG
  2     908   73.1         215    2  JE0242   Ig kappa chain NIG
  3     876   70.5         215    2  JE0243   Ig kappa chain NIG
  4     860   69.2         215    2  A23746   Ig kappa chain V-I
  5   841.5   67.8         216    2  JE0241   Ig kappa chain Am3
  6     820   66.0         219    2  S52028   Ig kappa chain - m
  7     807   65.0         219    2  PC4203   Ig kappa chain (mo
  8     806   64.9         219    2  S16112   Ig kappa chain V r
  9     796   64.1         219    2  S38865   Ig kappa chain - m
 10     795   64.0         217    2  S42772   Ig kappa chain - m
 11     770   62.0         225    2  JL0029   Ig kappa chain pre
 12   765.5   61.6         240    2  S06084   Ig kappa chain pre
 13   723.5   58.3         220    2  A31790   Ig kappa chain V r
 14     702   56.5         225    2  S37484   Ig kappa chain - m
 15   694.5   55.9         218    2  S68241   Ig kappa chain V r
 16   688.5   55.4         214    2  S68212   Ig kappa chain (Ma
 17   688.5   55.4         218    2  JC5810   monoclonal antibod
 18   688.5   55.4         234    2  S14237   Ig kappa chain pre
 19     686   55.2         197    2  S29593   Ig kappa chain (WM
 20   684.5   55.1         234    2  S01320   Ig kappa chain pre
 21     680   54.8         230    2  S33161   Ig kappa chain - s
 22   662.5   53.3         210    2  A56169   Ig kappa chain V r
 23     644   51.9         235    2  S25058   Ig kappa chain - m
 24     617   49.7         178    2  PT0219   Ig kappa chain V-C
 25     599   48.2         135    2  S52059   JC-kappa protein -
 26     572   46.1         229    2  A20969   Ig kappa chain pre
 27   565.5   45.5         140    2  S22658   Ig kappa chain pre
 28     552   44.4         133    2  S23230   Ig kappa chain pre
 29     552   44.4         133    2  S42611   HUNVK protein prec
 30     552   44.4         136    2  S40357   Ig kappa chain V-J
 31     550   44.3         133    1  K2HURP   Ig kappa chain pre
 32     549   44.2         133    2  S40324   Ig kappa chain C r
 33     548   44.1         106    2  K3HU     Ig kappa chain V r
 34     548   44.1         142    2  S22902   Ig kappa chain V r
 35     541   43.6         135    2  S40342   Ig kappa chain - h
 36     538   43.3         133    2  A24452   Ig kappa chain pre
 37     537   43.2         132    2  S26882   Ig kappa chain V r
 38     534   43.0         128    2  S40373   Ig kappa chain - h
 39     533   42.9         238    2  A49633   Ig lambda-like cha
 40     524   42.2         126    2  S40312   Ig kappa chain - h
 41     520   41.9         132    2  S40322   Ig kappa chain - h
 42   519.5   41.8         131    2  S40355   Ig kappa chain - h
 43     513   41.3         99     2  A37927   Ig kappa chain C r
 44   510.5   41.1         144    2  PL0106   Ig kappa chain pre
 45   508.5   40.9         132    2  PH0106   anti-digoxin trans
```

```
                           ALIGNMENTS

RESULT 1
JE0244
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match             73.7%;  Score 915;  DB 2;  Length 215;
Best Local Similarity   80.9%;  Pred. No. 2e-55;
Matches  178;  Conservative  19;  Mismatches  17;  Indels   6;  Gaps   3;

Qy       21 EVVMTQSPLSLPITPGEPASISCRSSQLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
            | |::|||||: :|||| |:|| :::||| || :|::||:|| :|||||:|||::| |:
Db        1 EVVLTQSPATLSVSPGERATLSCRASQSV-HSN---LAWYQQKPGQAPRLLIYRASTRA 55

Qy       81 SGVPDRRSGSGAGTDFTLKISAVEAEDVGYYFCGQGTRTPP-TFGGGTKVEIKRTVAAPS 139
            ::|:|||||| ||| |||| :|::::|:  |:: |||  | || ||||||||||||||
Db       56 TGIPARFSGSGSGTDFILTISSLQSEDFALYYCQQYNTWPLTFGGGTKVEIKRTVAAPS 115

Qy      140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 199
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      116 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 175

Qy      200 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
            ||||||||||||||||||||||||||||||||||||||||
Db      176 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2
JE0242
Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis:
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
Query Match   69.2%;   Score 860; DB 2; Length 215;
Best Local Similarity 78.4%;   Pred. No. 1.1e-51;
Matches 171; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

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Qy,  21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
            :|:|||:.:|:.:|||  ||:|||:   |||:   ||::  :||||||  |:|
Db    1 EIVLTQSPATLSLSPGERATLSGGASQSV----SSNYLAWYQQKPGQAPRLLIYDASSRA 56

Qy   81 SGVPDRFSGSGSGAGTDFTLKISAVEAEDVGYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
           :|:||||||||| || :|  |: |: |  ||.||:|||.|||  |:||||||||:|||:
Db   57 TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYGQQYGSSPLFFGGGTKVEIKRTVAAPSV 116

Qy  141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176

Qy  201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 238
           ||||||||||||||||| |||:||||||||||||||||
Db  177 SSTLTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE 214
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RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0241
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID; November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis:
A;Reference number: JE0241
A;Accession: JE0241
A;Molecule type: protein
A;Residues: 1-216 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>
Query Match   67.8%;   Score 841.5; DB 2; Length 216;
Best Local Similarity 76.7%;   Pred. No. 2e-50;
Matches 168; Conservative 21; Mismatches 27; Indels 3; Gaps 3;

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Qy   21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
            :|:|||:.:|:.:|||  ||:||||||||||||||:   ||::  :|||  |:|
Db    1 DIVLTQSPDFLAVSLGERATINCKSSQSVLY-NSKNFLAWYQQKPGQ-PKLLIW-ANVRE 57

Qy   81 SGVPDRFSGSGSGAGTDFTLKISAVEAEDVGYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
           :|:||||:|||||| ||| :|  |: |  ||.||:   |  : ::|||||||||:||||
Db   58 SGVPDRFRGSGVGTDFTLTIISNLQAELVAVYYCQQYSTPYSFSFQGGRLEIKRTVAAPSV 117

Qy  141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  118 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 177

Qy  201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
           ||||||||||||||||||||||||||||||||||||||
Db  178 SSTTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
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RESULT 6
S52028
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52028
R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Rooslen, J.; Dirkse, W.G.; Schots, A
submitted to the EMBL Data Library; August 1994
A;Description: Coordinate expression of antibody subunit genes yields high levels of
A;Reference number: S52028
A;Accession: S52028

RESULT 3
JE0243
Ig kappa chain NIG93 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0243
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID; November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0243
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
Query Match   73.1%;   Score 908; DB 2; Length 215;
Best Local Similarity 79.9%;   Pred. No. 5.9e-55;
Matches 175; Conservative 19; Mismatches 21; Indels 4; Gaps 1;

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Qy   21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
            :|:|||:.:|:.:|||  ||:||| :: :||:  :  :|::  :||||||  |:|
Db    1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNN----YLAWYQQKPGQAPSLLIYDASSRA 56

Qy   81 SGVPDRFSGSGSGAGTDFTLKISAVEAEDVGYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
           :|:||||||||| || :|  |: |: |  ||.||:|||  :  :::||||||||:|||:
Db   57 TGIPDRFSGSGSGTDFILTISGLEPEDFAVYYCQYDRPWTFGQGTKVEIKRTVAAPSV 116

Qy  141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176

Qy  201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
           |||||||||||||||||||||||||||||||||||||||
Db  177 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 4
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2835-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
Query Match   70.5%;   Score 876; DB 2; Length 215;
Best Local Similarity 77.7%;   Pred. No. 8.9e-53;
Matches 171; Conservative 18; Mismatches 25; Indels 6; Gaps 2;

```
Qy   21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
            :|:|||:.:|:.:|||  ||:||| :: :||:    TNVVWYMQKLGQAPRLLIYDASTRA 55
Db    1 EIVMTQSPAILSVSPGERATLSCRASQSVA----TNVVWYMQKLGQAPRLLIYDASTRA 55

Qy   81 SGVPDRFSGSGSGAGTDFTLKISAVEAEDVGYFCGQGTRTPPTFGGGTKVEIK-RTVAAPS 139
           :|:||||||||| || :|  |: |: |  ||.||:|||  :  :::||||||  ||||||
Db   56 TGVPARFSGSGSGTDFTLTISSLQSEDFAIYYCQHNAWPPTFGQGIKVETKKRTVAAPS 115

Qy  140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 199
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  116 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 175

Qy  200 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
           |||||||||||||||||||||||||||||||||||||||
Db  176 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
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          GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:   October  2, 2003, 08:56:23 ; Search time 6.59233 Seconds
                                       (without alignments)
                               1704.917 Million cell updates/sec

Title:         US-09-758-173-6
Perfect score: 1242
Sequence:      1 MSLPAQLLGLLLLCVPGSSG.........EVTHQGLSSPVTKSFNRGEC 239

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:        127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     SwissProt_41:*

                         SUMMARIES
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	550	44.3	133	1	KV2F_HUMAN	P06310 homo sapien
2	548	44.1	106	1	KAC_HUMAN	P01834 homo sapien
3	487	39.2	117	1	KV2E_HUMAN	P06309 homo sapien
4	471	37.9	113	1	KV2G_MOUSE	P01631 mus musculu
5	453	36.5	113	1	KV2D_HUMAN	P01617 homo sapien
6	433.5	34.9	112	1	KV2C_HUMAN	P01616 homo sapien
7	430	34.6	113	1	KV2B_HUMAN	P01615 homo sapien
8	422	34.0	129	1	KV3L_HUMAN	P18135 homo sapien
9	420.5	33.9	115	1	KV2A_HUMAN	P01614 homo sapien
10	420	33.8	133	1	KV4B_HUMAN	P06313 homo sapien
11	414	33.3	129	1	KV3H_HUMAN	P04207 homo sapien
12	414	33.3	129	1	KV3M_HUMAN	P18136 homo sapien
13	411.5	33.1	134	1	KV4C_HUMAN	P06314 homo sapien
14	404	32.5	113	1	KV2E_MOUSE	P03976 mus musculu
15	403.5	32.5	131	1	KV3I_MOUSE	P01661 mus musculu
16	401	32.3	113	1	KV2F_MOUSE	P01630 mus musculu
17	399.5	32.2	132	1	KV3F_MOUSE	P01658 mus musculu
18	396.5	31.9	128	1	KV3K_HUMAN	P05311 homo sapien
19	389	31.3	112	1	KV2D_MOUSE	P01629 mus musculu
20	384.5	31.0	114	1	KV4A_HUMAN	P01625 homo sapien
21	372.5	30.0	115	1	KV3I_HUMAN	P04433 homo sapien
22	372	30.0	109	1	KV3D_HUMAN	P01622 homo sapien
23	369.5	29.8	121	1	KV4O_HUMAN	P06312 homo sapien
24	368.5	29.7	111	1	KV3H_MOUSE	P01660 mus musculu
25	368.5	29.7	136	1	KV5B_MOUSE	P01634 mus musculu
26	368	29.6	113	1	KV2C_MOUSE	P01628 mus musculu
27	367	29.5	106	1	KACB_RAT	P01835 rattus norv
28	364.5	29.3	111	1	KV3M_MOUSE	P01665 mus musculu
29	364.5	29.3	111	1	KV3O_MOUSE	P01667 mus musculu
30	364	29.3	109	1	KV3B_HUMAN	P01620 homo sapien
31	364	29.3	120	1	KV2B_MOUSE	P01627 mus musculu
32	363.5	29.3	111	1	KV3N_MOUSE	P01666 mus musculu
33	361	29.1	109	1	KV3F_HUMAN	P01624 homo sapien
34	359.5	28.9	108	1	KV1_CANFA	P01618 canis famil
35	359	28.9	106	1	KACA_RAT	P01836 rattus norv
36	358.5	28.9	111	1	KV3J_MOUSE	P01662 mus musculu
37	358	28.8	110	1	KV3P_MOUSE	P01668 mus musculu
38	357.5	28.8	111	1	KV3C_MOUSE	P01656 mus musculu
39	357.5	28.8	111	1	KV3Q_MOUSE	P01669 mus musculu
40	356.5	28.7	111	1	KV3T_MOUSE	P01672 mus musculu
41	354.5	28.5	111	1	KV3L_MOUSE	P01664 mus musculu
42	354.5	28.5	111	1	KV3R_MOUSE	P01670 mus musculu
43	354.5	28.5	129	1	KV1W_HUMAN	P04431 homo sapien
44	354	28.5	109	1	KV3E_HUMAN	P01623 homo sapien
45	353	28.4	112	1	KV2A_MOUSE	P01626 mus musculu

                         ALIGNMENTS

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RESULT 1
KV2F_HUMAN
ID   KV2F_HUMAN      STANDARD;       PRT;    133 AA.
AC   P06310;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-II region RPMI 6410 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041852; PubMed=2997711;
RA   Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III.";
RL   Nucleic Acids Res. 13:6499-6513(1985).
CC   -!- -----------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -!- -----------------------------------------------------------------
DR   EMBL; Z00020; CAA77315.1; -.
DR   PIR; A01890; K2HURP.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    133       IG KAPPA CHAIN V-II REGION RPMI 6410.
FT   DOMAIN       21    133       FRAMEWORK-1.
FT   DOMAIN       44     59       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       60     74       FRAMEWORK-2.
FT   DOMAIN       75     81       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       82    113       FRAMEWORK-3.
FT   DOMAIN      114    122       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      123    132       FRAMEWORK-4.
FT   DISULFID     43    113       BY SIMILARITY.
FT   NON_TER     133    133
SQ   SEQUENCE   133 AA;  14707 MW;  513CCAF3673009EE CRC64;
```

Query Match   44.3%;   Score 550; DB 1; Length 133;
Best Local Similarity   80.5%;   Pred. No. 1.8e-37;

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Matches 107;  Conservative 13;  Mismatches 13;  Indels  0;  Gaps   0;

Qy    1 MSLPAQLLGILLLCVPGSSGEVVMTQSPSLSLPITPGEPASISCRSSQSLKHSNGDTFLSW  60
          :|||||||: ||||||:|||||:|||||||||  :||||||||||  :|:|:|:|
Db    1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW  60

Qy   61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSGAGTDFTLKISAVEAEDVGVYFCGQGIRTP 120
          ::|:|| || ||||||||||||||||||||:|||||||||| :||||||||||:| |||
Db   61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYTCMQGTHWS 120

Qy  121 PTFGGGTKVEIKR 133
          ||| ||||||||
Db  121 WTFGQGTKVEIKR 133


RESULT 2
KAC_HUMAN
ID   KAC_HUMAN      STANDARD;      PRT;   106 AA.
AC   P01834;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig kappa chain C region.
GN   IGKC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (MYELOMA PROTEIN EU).
RX   MEDLINE=71064023; PubMed=5489770;
RA   Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT   acid sequence of the light chain.";
RL   Biochemistry 9:3155-3161(1970).
RN   [2]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [3]
RP   SEQUENCE (BENCE-JONES PROTEIN TI).
RX   MEDLINE=72188439; PubMed=5027703;
RA   Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT   Ti). IV. The complete amino acid sequence and its significance for
RT   the mechanism of antibody production.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81042304; PubMed=6775818;
RA   Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT   "Cloned human and mouse kappa immunoglobulin constant and J region
RT   genes conserve homology in functional segments.";
RL   Cell 22:197-207(1980).
RN   [5]
RP   SEQUENCE (BENCE-JONES PROTEIN ROY).
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RT   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press,
RL   New York (1969).
RN   [6]
RP   SEQUENCE (BENCE-JONES PROTEIN CUM).
RX   MEDLINE=68242259; PubMed=5586923;
RA   Hilschmann N.;
RT   "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT   type).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN   [7]
RP   SEQUENCE (BENCE-JONES PROTEIN AG).
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
RN   [8]
RP   SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX   MEDLINE=70201507; PubMed=5447531;
RA   Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT   "Macroglobulin structure: variable sequence of light and heavy
RT   chains.";
RL   Science 169:56-59(1970).
RN   [9]
RP   SEQUENCE OF 1-33; 38-41 AND 62-80.
RC   TISSUE=Abdominal adipose tissue;
RX   PubMed=9588180;
RA   Olsen K.E., Sletten K., Westermark P.;
RT   "Extended analysis of AL-amyloid protein from abdominal wall
RT   subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL   Biochem. Biophys. Res. Commun. 245:713-716(1998).
-!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC       45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1.2) ALLOTYPIC
CC       MARKER, 45-ALA AND 83-LEU.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   -----------------------------------------------------------------------
DR   EMBL; J00241; AAA58989.1; -.
DR   EMBL; V00557; CAA23823.1; -.
DR   PIR; B90552; K3HU.
DR   PDB; 1D5B; 09-FEB-00.
DR   PDB; 1D5I; 09-FEB-00.
DR   PDB; 1D6V; 04-OCT-00.
DR   PDB; 1HEZ; 10-AUG-01.
DR   PDB; 1HKL; 12-MAR-97.
DR   PDB; 1I72; 08-AUG-01.
DR   PDB; 1MIM; 15-MAY-97.
DR   Genew; HGNC:5716; IGKC.
DR   MIM; 147200; -.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        5    102                   IG-LIKE.
FT   DISULFID     26     86
FT   DISULFID    106    106                   INTERCHAIN (WITH A HEAVY CHAIN).
FT   VARIANT      83     83                   V -> L (IN INV(1.2) MARKER).
FT                                            /FTId=VAR_003897.
FT   CONFLICT     14     14                   D -> N (IN REF. 7 AND 8).
FT   CONFLICT     57     57                   E -> Q (IN REF. 5 AND 6).
SQ   SEQUENCE   106 AA;  11609 MW;  51984D1FDD372CE8 CRC64;

Query Match             44.1%;  Score 548;  DB 1;  Length 106;
Best Local Similarity   100.0%;  Pred. No. 2e-37;
Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy  134 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 193
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS  60
```

OM protein - protein search, using sw model

```
              GenCore version 5.1.6
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Run on:    October  2, 2003,  08:56:23 ; Search time 23.129 seconds
                                          (without alignments)
                                          2666.544 Million cell updates/sec

Title:         US-09-758-173-6
Perfect score: 1242
Sequence: 1 MSLPAQLLGLLLCVPGSSG........EVTHQGLSSPVTKSFNRGEC 239
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched:      830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:     830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SPTREMBL_23:*
    1: sp_archea:*
    2: sp_bacteria:*
    3: sp_fungi:*
    4: sp_human:*
    5: sp_invertebrate:*
    6: sp_mammal:*
    7: sp_mhc:*
    8: sp_organelle:*
    9: sp_phage:*
   10: sp_plant:*
   11: sp_rodent:*
   12: sp_virus:*
   13: sp_vertebrate:*
   14: sp_unclassified:*
   15: sp_rvirus:*
   16: sp_bacteriap:*
   17: sp_archeap:*
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1103	88.8	239	4	Q8TCD0	Q8tcd0 homo sapien
2	1086	87.4	239	4	Q8NEK0	Q8nek0 homo sapien
3	949.5	76.4	234	4	Q8NEK1	Q8nek1 homo sapien
4	864.5	69.6	238	11	Q8VCI6	Q8vci6 mus musculu
5	843.5	67.9	238	11	Q99M37	Q99m37 mus musculu
6	808	65.1	239	11	Q8VC55	Q8vc55 mus musculu
7	792	63.8	239	11	Q8K0F8	Q8k0f8 mus musculu
8	691.5	55.7	234	11	Q8VCP0	Q8vcp0 mus musculu
9	682.5	55.0	234	11	Q91WF8	Q91wf8 mus musculu
10	669.5	53.9	234	11	Q8R062	Q8r062 mus musculu
11	667	53.7	235	11	Q91W12	Q91w12 mus musculu
12	656.5	52.9	234	11	Q8R028	Q8r028 mus musculu
13	655.5	52.8	233	11	Q91WS9	Q91ws9 mus musculu
14	638.5	51.4	214	11	Q9R1A5	Q9r1a5 mus musculu
15	462.5	37.2	114	4	Q9UL80	Q9ul80 homo sapien
16	460.5	37.1	233	4	Q8TBC9	Q8tbc9 homo sapien
17	447	36.0	234	4	Q8N355	Q8n355 homo sapien
18	445	35.8	236	4	Q8NEJ1	Q8nej1 homo sapien
19	437.5	35.2	237	4	Q8WTU6	Q8wtu6 homo sapien
20	434.5	35.0	237	4	Q8WUK4	Q8wuk4 homo sapien
21	427	34.4	104	11	Q9JL82	Q9jl82 mus musculu
22	414.5	33.4	233	4	Q8N5F4	Q8n5f4 homo sapien
23	408	32.9	236	4	Q96E61	Q96e61 homo sapien
24	407.5	32.8	148	11	Q8K122	Q8k122 mus musculu
25	380	30.6	235	11	Q99M11	Q99m11 mus musculu
26	379.5	30.2	233	4	Q96I69	Q96i69 homo sapien
27	375	30.2	109	4	Q9UL78	Q9ul78 homo sapien
28	362.5	29.2	240	4	Q8WUK3	Q8wuk3 homo sapien
29	353.5	28.5	111	11	Q920E9	Q920e9 mus musculu
30	350	28.2	109	4	Q9UL85	Q9ul85 homo sapien
31	342.5	27.6	108	4	Q9UL83	Q9ul83 homo sapien
32	342	27.5	109	4	Q9UL86	Q9ul86 homo sapien
33	333.5	26.9	107	4	Q9ER29	Q9erz9 mus musculu
34	329.5	26.5	103	11	Q9JL80	Q9jl80 mus musculu
35	329.5	26.5	108	4	Q9UL79	Q9ul79 homo sapien
36	326	26.2	134	4	Q8VDD0	Q8vdd0 homo sapien
37	324	26.1	107	4	Q96SA9	Q96sa9 homo sapien
38	324	26.1	114	4	Q8K1F1	Q8k1f1 mus musculu
39	322.5	26.0	108	4	Q9UL77	Q9ul77 homo sapien
40	321	25.8	112	11	Q8K1F3	Q8k1f3 mus musculu
41	314.5	25.3	108	4	Q9UL70	Q9ul70 homo sapien
42	314	25.3	112	11	Q8K1F2	Q8k1f2 mus musculu
43	312.5	25.2	99	11	Q9JL74	Q9jl74 mus musculu
44	309.5	24.9	298	11	Q9QYF0	Q9qyf0 mus musculu
45	309	24.9	107	4	Q9UL81	Q9ul81 homo sapien

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

```
RESULT 1
Q8TCD0
ID   Q8TCD0;            PRELIMINARY;     PRT;    239 AA.
AC   Q8TCD0;
DT   01-JUN-2002 (TREMBLrel. 21, Created)
DT   01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022362; AAH22362.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   239 AA;   26234 MW;   FACEDC3A3B03871D CRC64;

Query Match             88.8%;  Score 1103;  DB 4;  Length 239;
Best Local Similarity   88.7%;  Pred. No. 3.6e-93;
Matches  212;  Conservative  15;  Mismatches  12;  Indels  0;  Gaps  0;

Qy     1 MSLPAQLLGLLLCVPGSSGGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW  60
           ||||||||||:|:||||||| :|||||||||:|:: |:|||||||:||:|:::||: |:|
Db     1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSTQSLVVSDGNTYLNW  60

Qy    61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
           :||:|||.||:|||||||||||||||||||||.|||||||::||||||||||||:|| :|
Db    61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTHWP 120
```

Qy 121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
         ||.:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 STFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180

Qy 181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSSPVTKSFNRGEC 239
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSSPVTKSFNRGEC 239

RESULT 2
Q8NEK0
ID   Q8NEK0   PRELIMINARY;   PRT;   239 AA.
AC   Q8NEK0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC030814; AAH30814.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match   87.4%; Score 1086; DB 4; Length 239;
Best Local Similarity   87.9%; Pred. No. 1.3e-91;
Matches 210; Conservative 11; Mismatches 18; Indels   0; Gaps   0;

Qy   1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
         |.|||||||||.||.|||||:::||||||||||:|||||||||||||||||.|.:.:.|
Db   1 MRLPALLGLLMLWVSGSSGDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDW 60

Qy   61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGYFCGQGTRTP 120
         |.||||||.|.|||| |.||||||||||||||:|||||||||.|||||||:.|:|||||
Db   61 YLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISKVEAEDVGIYYCMQGLQTP 120

Qy 121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
         .|||.||||||||||||||||||||||||||||||||||||||||||||||||||||.||
Db 121 QTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNTLQ 180

Qy 181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSSPVTKSFNRGEC 239
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSSPVTKSFNRGEC 239

RESULT 3
Q8NEK1
ID   Q8NEK1   PRELIMINARY;   PRT;   234 AA.
AC   Q8NEK1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;

RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC030813; AAH30813.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 234 AA; 25530 MW; 6316E8DF8D132F8 CRC64;

Query Match   76.4%; Score 949.5; DB 4; Length 234;
Best Local Similarity   77.8%; Pred. No. 4.3e-79;
Matches 186; Conservative 24; Mismatches 24; Indels   5; Gaps   2;

Qy   1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
         |.|||||||.||||.||||||:::|||||||:.||||||||||||||.:.:|.||:||
Db   1 MEAPAQLLFLLLLWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVT-SN---LAW 55

Qy   61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGYFCGQGTRTP 120
         |||.|||:||||::|..:|:|||||:|||||:.|||||:||::||:||.|:|||.:..|
Db   56 YQQTPGQSPRLVIYGASSRASGVPARFSGSGSGTEFTLTISSLQSEDFAVYYCCQYNKWP 115

Qy 121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
         .||||||| :|||||||||||||||||||||||||||||||||||||||||||||||.||
Db 116 HTFGGGTKLDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 175

Qy 181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSSPVTKSFNRGEC 239
         |||||||||||||||||||||||||||||||||||||||.||||||||||||||||||||
Db 176 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSSPVTKSFNRGEC 234

RESULT 4
Q8VCI6
ID   Q8VCI6   PRELIMINARY;   PRT;   238 AA.
AC   Q8VCI6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical 26.2 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019760; AAH19760.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match   69.6%; Score 864.5; DB 11; Length 238;
Best Local Similarity   68.2%; Pred. No. 2.8e-71;
Matches 163; Conservative 30; Mismatches 45; Indels   1; Gaps   1;

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Db   1 MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHW 59

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 09:12:09 ; Search time 10.6148 Seconds
(without alignments)
952.662 Million cell updates/sec

Title: US-09-758-173-6
Perfect score: 1242
Sequence: 1 MSLPAQLLGLLLLCVPGSSG.........EVTHQGLSSPVTKSFNRGEC 239

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1242	100.0	239	3	US-08-487-550-6	Sequence 6, Appli
2	1242	100.0	239	4	US-09-526-098-6	Sequence 6, Appli
3	978	78.7	241	1	US-07-916-098A-56	Sequence 56, Appli
4	976	78.6	242	1	US-08-398-613A-56	Sequence 56, Appl
5	976	78.6	242	1	US-08-398-612A-56	Sequence 56, Appl
6	976	78.6	242	1	US-08-398-611A-56	Sequence 56, Appl
7	976	78.6	242	3	US-08-491-334A-56	Sequence 56, Appl
8	976	78.6	242	3	US-09-027-449-42	Sequence 42, Appl
9	976	78.6	242	3	US-08-804-444A-42	Sequence 42, Appl
10	976	78.6	242	4	US-09-026-985-42	Sequence 42, Appl
11	976	78.6	242	4	US-09-121-952A-42	Sequence 42, Appl
12	976	78.6	242	4	US-09-234-340A-42	Sequence 42, Appl
13	975.5	78.5	234	3	US-09-301-593-36	Sequence 36, Appl
14	939.5	75.6	242	3	US-09-049-672A-6	Sequence 6, Appli
15	936	75.4	242	3	US-09-027-449-62	Sequence 62, Appl
16	936	75.4	242	4	US-09-026-985-62	Sequence 62, Appl
17	936	75.4	242	4	US-09-121-952A-62	Sequence 62, Appl
18	936	75.4	242	4	US-09-234-340A-62	Sequence 62, Appl
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20	935	75.3	242	3	US-08-804-444A-51	Sequence 51, Appl
21	935	75.3	242	4	US-09-026-985-51	Sequence 51, Appl
22	935	75.3	242	4	US-09-121-952A-51	Sequence 51, Appl
23	935	75.3	242	4	US-09-234-340A-51	Sequence 51, Appl
24	932	75.0	219	3	US-09-027-449-72	Sequence 72, Appl
25	932	75.0	219	4	US-09-026-985-72	Sequence 72, Appl
26	932	75.0	219	4	US-09-121-952A-72	Sequence 72, Appl
27	932	75.0	219	4	US-09-234-340A-72	Sequence 72, Appl
28	932	75.0	242	3	US-09-027-449-56	Sequence 56, Appl
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30	932	75.0	242	3	US-09-026-985-56	Sequence 56, Appl
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32	932	75.0	242	4	US-09-234-340A-56	Sequence 56, Appl
33	928.5	74.8	240	4	US-09-301-593-28	Sequence 28, Appl
34	909.5	73.2	220	3	US-08-952-235-1	Sequence 1, Appli
35	909.5	73.2	220	4	US-09-669-971-1	Sequence 1, Appli
36	904.5	72.8	234	4	US-09-740-002-24	Sequence 24, Appl
37	900.5	72.5	235	3	US-08-812-586-16	Sequence 16, Appl
38	900.5	72.5	235	3	US-09-535-832A-17	Sequence 17, Appl
39	900	72.5	235	1	US-08-276-852-153	Sequence 153, App
40	900	72.5	235	1	US-08-899-575-153	Sequence 153, App
41	900	72.5	235	1	US-08-899-575-153	Sequence 153, App
42	900	72.5	235	5	PCT-US95-08743-153	Sequence 153, App
43	899.5	72.4	236	1	US-08-157-101A-5	Sequence 5, Appli
44	893.5	71.9	218	5	PCT-US96-13152-2	Sequence 2, Appli
45	893.5	71.9	220	4	US-09-301-593-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-6
; Sequence 6, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMONOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-6

Query Match 100.0%; Score 1242; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.9e-101;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLPAQLLGLLLLCVPGSSGGEVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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Qy   181  SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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RESULT 2
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; Sequence 6, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/526,098
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 239 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-526-098-6

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Best Local Similarity   100.0%; Pred. No. 3.9e-101;
Matches 239; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   121  PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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RESULT 3
US-07-916-098A-56
; Sequence 56, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
;   APPLICANT: BURKLY, LINDA C.
;   APPLICANT: CHISHOLM, PATRICIA L.
;   APPLICANT: THOMAS, DAVID W.
;   APPLICANT: ROSA, MARGARET D.
;   APPLICANT: ROSA, JOSEPH J.
;   TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;   TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;   NUMBER OF SEQUENCES: 61
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
;   STREET: 10 SOUTH WACKER DRIVE
;   CITY: CHICAGO
;   STATE: ILLINOIS
;   COUNTRY: U.S.A.
;   ZIP: 60606
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/916,098A
;   FILING DATE: July 24, 1992
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US91/08843
;   FILING DATE: No. 5871732ember 27, 1991
;   CLASSIFICATION: 424
;   APPLICATION NUMBER: 07/618,542
;   FILING DATE: No. 5871732ember 27, 1990
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: JOHN J. MC DONNELL
;   REGISTRATION NUMBER: 26,949
;   REFERENCE/DOCKET NUMBER: 92,310-G
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (312) 715-1000
;   TELEFAX: (312) 715-1234
;   TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 56:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 241 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-07-916-098A-56

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Qy    60  WYQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRT 119
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Qy   120  PPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 179
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                GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:  October  2, 2003, 09:18:44 ; Search time 89.7228 Seconds
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Title:           US-09-758-173-6
Perfect score:   1242
Sequence:        1 MSLPAQLGLILLCVPGSSG.........EVTHQGLSSPVTKSFNRGEC 239

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Searched:        587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters:        587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Database :       Published_Applications_AA:*
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                11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1242	100.0	239	10	US-09-948-429B-6	Sequence 6, Appli
2	1242	100.0	239	12	US-10-124-807-6	Sequence 6, Appli
3	1242	100.0	239	12	US-10-291-532-6	Sequence 6, Appli
4	1242	100.0	239	14	US-10-124-905-6	Sequence 6, Appli
5	1068	86.0	239	11	US-09-992-600A-8	Sequence 8, Appli
6	1068	86.0	239	12	US-09-924-340-8	Sequence 8, Appli
7	1068	86.0	239	12	US-10-154-678-8	Sequence 8, Appli
8	1068	86.0	239	12	US-09-992-095B-8	Sequence 8, Appli
9	1068	86.0	239	12	US-09-999-570-8	Sequence 8, Appli
10	1068	86.0	239	15	US-10-000-489-8	Sequence 8, Appli
11	1068	86.0	239	15	US-10-000-986-8	Sequence 8, Appli
12	1008	81.2	219	11	US-09-972-656-92	Sequence 92, Appl
13	1003.5	80.8	238	15	US-10-171-452A-38	Sequence 38, Appl
14	1003.5	80.8	238	15	US-10-171-452A-56	Sequence 56, Appl
15	997	80.3	219	11	US-09-972-656-106	Sequence 106, App
16	993.5	80.0	238	15	US-10-171-452A-44	Sequence 44, Appl
17	993.5	80.0	238	15	US-10-171-452A-50	Sequence 50, Appl
18	992.5	79.9	220	10	US-09-822-698A-24	Sequence 24, Appl
19	991	79.8	219	11	US-09-972-656-104	Sequence 104, App
20	977	78.7	219	11	US-09-972-656-94	Sequence 94, Appl
21	976.5	78.6	238	12	US-10-384-933-107	Sequence 107, App
22	976.5	78.6	238	15	US-10-216-484-107	Sequence 107, App
23	976	78.6	242	11	US-09-726-258-42	Sequence 42, Appl
24	975.5	78.5	240	12	US-10-159-006-36	Sequence 36, Appl
25	971.5	78.2	238	12	US-10-388-933-109	Sequence 109, App
26	971	78.2	238	15	US-10-216-484-109	Sequence 109, App
27	970.5	78.1	238	12	US-10-384-933-54	Sequence 54, Appl
28	970.5	78.1	238	15	US-10-216-484-54	Sequence 54, Appl
29	969	78.0	235	15	US-10-153-382-7	Sequence 7, Appli
30	965.5	77.7	238	12	US-10-384-933-52	Sequence 52, Appl
31	965.5	77.7	238	15	US-10-216-484-52	Sequence 52, Appl
32	964.5	77.7	238	12	US-10-384-933-50	Sequence 50, Appl
33	964.5	77.7	238	15	US-10-216-484-50	Sequence 50, Appl
34	963	77.5	233	15	US-10-153-382-11	Sequence 11, Appl
35	960.5	77.3	228	11	US-09-909-567B-50	Sequence 50, Appl
36	960	77.3	239	10	US-09-249-011A-22	Sequence 22, Appl
37	958.5	77.2	239	10	US-10-171-452A-39	Sequence 39, Appl
38	958.5	77.1	218	15	US-10-171-452A-57	Sequence 57, Appl
39	957.5	77.1	234	12	US-10-153-382-15	Sequence 15, Appl
40	955.5	76.9	234	12	US-10-225-108A-4	Sequence 4, Appli
41	955	76.9	234	12	US-09-848-832-4	Sequence 4, Appli
42	954.5	76.9	240	9	US-09-799-514-8	Sequence 8, Appli
43	948.5	76.4	218	15	US-10-171-452A-45	Sequence 45, Appl
44	948.5	76.4	218	15	US-10-171-452A-51	Sequence 51, Appl
45	948.5	76.4	238	12	US-10-384-933-129	Sequence 129, App

ALIGNMENTS

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RESULT 1
US-09-948-429B-6
; Sequence 6, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/948,429B
;   FILING DATE:
;   CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
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;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 239 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-948-429B-6

Query Match             100.0%;   Score 1242;   DB 10;   Length 239;
Best Local Similarity   100.0%;   Pred. No. 7.2e-78;
Matches  239;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

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Qy   61  YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP  120

Qy  121  PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ  180
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Db  121  PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ  180

Qy  181  SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC  239
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC  239


RESULT 2
US-10-124-807-6
; Sequence 6, Application US/10124807
; Publication No. US20030166207A1
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;     STREET: 699 Prince Street
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22314
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/124,807
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/383,916
;     FILING DATE:
;     APPLICATION NUMBER: US 08/487,550
;     FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Teskin, Robin L.
;     REGISTRATION NUMBER: 35,030
;     REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-836-6620
;     TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 239 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-10-124-807-6

Query Match             100.0%;   Score 1242;   DB 12;   Length 239;
Best Local Similarity   100.0%;   Pred. No. 7.2e-78;
Matches  239;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

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Db    1  MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW  60

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Db   61  YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP  120

Qy  121  PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ  180
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RESULT 3
US-10-291-532-6
; Sequence 6, Application US/10291532
; Publication No. US2003018029OA1
; GENERAL INFORMATION:
;   APPLICANT: HARIHARAN, KANDASAMY
;   APPLICANT: HANNA, NABIL
;   TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
;   TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
;   TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
;   FILE REFERENCE: 037003/291872
;   CURRENT APPLICATION NUMBER: US/10/291,532
;   CURRENT FILING DATE: 2002-11-12
;   PRIOR APPLICATION NUMBER: 60/331,187
;   PRIOR FILING DATE: 2001-11-09
;   PRIOR APPLICATION NUMBER: 09/758,173
;   PRIOR FILING DATE: 2001-01-12
;   PRIOR APPLICATION NUMBER: 09/383,916
;   PRIOR FILING DATE: 1999-08-26
;   PRIOR APPLICATION NUMBER: 08/487,950
;   PRIOR FILING DATE: 1995-06-07
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: primatized peptide sequence
US-10-291-532-6

Query Match             100.0%;   Score 1242;   DB 12;   Length 239;
Best Local Similarity   100.0%;   Pred. No. 7.2e-78;
Matches  239;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy    1  MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW  60
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Db    1  MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW  60

Qy   61  YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP  120
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Db   61  YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP  120

Qy  121  PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ  180
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: October 2, 2003, 13:01:50 ; Search time 3774.61 Seconds
(without alignments)
15574.362 Million cell updates/sec

Title: US-09-758-173-7
Perfect score: 1437
Sequence: 1 ATGGGTGGAGCCTCATCTT........CCCTGTCTCCGGTAAATGA 1437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
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2: gb_htg:*
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13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1437	100.0	1437	6	AR108865	AR108865 Sequence
2	1437	100.0	1437	6	AR265199	AR265199 Sequence
3	1437	100.0	1437	6	BD063037	BD063037 Identific
4	1238.6	86.2	1642	9	AK093806	AK093806 Homo sapi
5	1219	84.8	7521	6	AX080951	AX080951 Sequence
6	1208	84.1	1659	9	BC014667	BC014667 Homo sapi
7	1189.2	82.8	1666	9	BC006402	BC006402 Homo sapi
8	1188.2	82.7	1679	9	BC018747	BC018747 Homo sapi
9	1186.2	82.5	1630	9	BC024289	BC024289 Homo sapi
10	1185	82.5	1425	9	AY172959	AY172959 Homo sapi
11	1185	82.5	1430	6	AX419496	AX419496 Sequence
12	1184.6	82.4	1549	6	A21385	A21385 Plasmid DNA
13	1184	82.4	1673	9	HSIG1LH	Y14737 Homo sapien
14	1183.4	82.4	1633	9	AK097859	AK097859 Homo sapi
15	1183	82.3	1630	9	BC041037	BC041037 Homo sapi
16	1182.2	82.3	1990	9	AK098817	AK098817 Homo sapi
17	1177.8	82.0	19040	6	BD075127	BD075127 Method fo
18	1173	81.6	1631	9	AK097010	AK097010 Homo sapi
19	1171.8	81.5	3143	9	BC019046	BC019046 Homo sapi
20	1169.6	81.4	1624	9	HSIG1KH	Y14735 Homo sapien
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22	1162.2	80.9	1419	12	AF019036	AF019036 Synthetic
23	1157.4	80.5	1404	9	AF027159	AF027159 Homo sapi
24	1155	80.4	1627	9	AK097350	AK097350 Homo sapi
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26	1148.2	79.9	1624	9	AK097206	AK097206 Homo sapi
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29	1147.8	79.9	1392	6	AX616908	AX616908 Sequence
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31	1147.2	79.8	1335	6	AX010615	AX010615 Sequence
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38	1133.4	78.9	1599	6	AX330501	AX330501 Sequence
39	1133.4	78.9	1599	6	AX333307	AX333307 Sequence
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42	1131.8	78.8	1617	6	A29585	A29585 H.sapiens c
43	1130.2	78.6	1449	6	BD078407	BD078407 Antigen-b
44 c	1130.2	78.6	1449	6	BD078408	BD078408 Antigen-b
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ALIGNMENTS

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LOCUS   AR108865   1437 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6113898.
ACCESSION   AR108865
VERSION   AR108865.1 GI:12825141
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1437)
  AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
  TITLE   Human B7.1-specific primatized antibodies and transfectomas
            expressing said antibodies
  JOURNAL   Patent: US 6113898-A 7 05-SEP-2000;

Pred. No. is the number of results predicted by chance to have a

FEATURES   Location/Qualifiers
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                /organism="unknown"
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ORIGIN

Query Match   100.0%;   Score 1437;   DB 6;   Length 1437;
Best Local Similarity   100.0%;   Pred. No. 1.3e-280;
Matches 1437;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db      1 ATGGGTTGGAGCCTCATCTTGCTTCTTCCTTGCTTGCTTACGCGTGTCCAGTGTGAG 60

Qy     61 GTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGTCCTGAGAGTCTCC 120
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Db     61 GTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGTCCTGAGAGTCTCC 120

Qy    121 TGTGCAGTCTCTGGATTCAGTGACCACTACCATGTCATGTCCGGCCAGCCTCCA 180
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Qy    301 TATCTGCAAATGAGCAGCCTGAAAATGCGAGGACACGGCCGTCTATTACTTGTACTACATCC 360
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Qy    361 TACAATTCACATTGTCGGGGGTGGTGTCTGCTATGGAGGTTACTTCGAATTCTCGGGGCCAG 420
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Qy    721 AAGGTTGAGCAGAGAAAGCAGAGCCCCAAATCTTGTGACAAAACTCACACAGCCCACCGTC 780
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAACCCAAGGAC 840

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(Second column)

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Qy   1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1080
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Qy   1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGTGTAC 1140
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Qy   1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
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RESULT 2
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LOCUS   AR265199   1437 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 7 from patent US 6492134.
ACCESSION   AR265199
VERSION   AR265199.1   GI:29693620
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1437)
  AUTHORS   Aquin,S. and Vezina,Louis.-P.
  TITLE   Method for producing polyhydroxyalkanoates in recombinant organisms
  JOURNAL   Patent: US 6492134-A 7 10-DEC-2002;
FEATURES   Location/Qualifiers
    source 1..1437
            /organism="unknown"
BASE COUNT   329 a   451 c   387 g   270 t
ORIGIN

Query Match   100.0%;   Score 1437;   DB 6;   Length 1437;
Best Local Similarity   100.0%;   Pred. No. 1.3e-280;
Matches 1437;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy      1 ATGGGTTGGAGCCTCATCTTGCTTCTTCCTTGCTTGCTTACGCGTGTCCAGTGTGAG 60
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Qy     61 GTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGTCCTGAGAGTCTCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGTCCTGAGAGTCTCC 120

Qy    121 TGTGCAGTCTCTGGATTCAGTGACCACTACCATGTCATGTCCGGCCAGCCTCCA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTGCAGTCTCTGGATTCAGTGACCACTACCATGTCATGTCCGGCCAGCCTCCA 180

Qy    181 GGGAAGGGGCCGGAATGGGTAGGTTTCATTAGAAACAAACCGAACGGTGGGACAACAGAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGAAGGGGCCGGAATGGGTAGGTTTCATTAGAAACAAACCGAACGGTGGGACAACAGAA 240
```

OM nucleic - nucleic search, using sw model

```
                 GenCore version 5.1.6
         Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:   October  2, 2003, 12:12:30 ; Search time 294.323 Seconds
                                        (without alignments)
                                        13179.730 Million cell updates/sec

Title:          US-09-758-173-7
Perfect score:  1437
Sequence:       1 ATGGGTTGGAGCCTCATCTT........CCCTGTCTCCGGGTAAATGA 1437

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       252756 seqs, 134971017 residues

Total number of hits satisfying chosen parameters:   5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  N_Geneseq_19Jun03:*
     1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
     2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
     3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
     4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
     5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
     6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
     7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
     8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
     9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
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    11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
    12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
    13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
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    16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
    17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
    18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
    19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
    20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
    21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
    22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
    23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
    24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
    25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
```

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	1437	100.0	1437	19	AAV35487	Macaque primatized
2	1437	100.0	1437	24	AAS17245	DNA sequence of a
3	1435.4	99.9	1437	18	AAT13847	Primatised anti-hu
4	1219	84.8	7521	22	AAF30315	Bicistronic chimer
5	1216	84.6	1616	24	AAS62785	cDNA sequence #572
6	1199.2	83.5	1386	14	AAQ49834	Anti-HIV-1 recombi
7	1186	82.5	1798	21	AAC98220	Human colon cancer
8	1185	82.5	1430	24	AAK98701	cDNA of the heavy
9	1185	82.5	1430	25	ABX12855	Human monoclonal r
10	1184	82.4	1644	22	AAS22593	Human cDNA encodin
11	1183	82.3	1549	19	AAQ20066	Encodes heavy chai
12	1182.2	82.3	19035	19	AAV61794	Traget plasmid Man
13	1178	82.0	1404	25	ABZ24633	Humanised 3D6 anti
14	1171.4	81.5	1427	19	AAV41431	Plasmid Hu19CHcpcd
15	1171.4	81.5	1427	19	AAV41432	Plasmid Hu19DHcpcd
16	1169.8	81.4	1427	19	AAV41429	Plasmid Hu19BHcpcd
17	1169.4	81.4	1442	22	AAC84208	Plasmid Glambda-1B
18	1166.2	81.2	6281	22	AAC84206	Plasmid Glambda-1A
19	1165.4	81.1	1615	22	ABK34973	Human cDNA encodin
20	1163	80.9	1617	24	AAS62784	cDNA sequence #571
21	1158.8	80.6	6284	19	AAV41427	Plasmid Hu19ARcpcd
22	1155.8	80.4	1576	14	AAQ49944	Human anti-HBs hea
23	1155.4	80.4	1641	15	AAQ54655	chiT84.12 H3 heavy
24	1153.4	80.3	2974	22	AAH98397	Synthetic EST-deri
25	1147.8	79.9	1392	25	AAD53212	BIWA4/8 antibody h
26	1147.8	79.9	9568	25	AAD53219	BIWA4 antibody DNA
27	1147.2	79.8	1335	21	AAZ34748	Humanised anti-CD2
28	1142.8	79.5	1598	24	ABK34965	Human cDNA encodin
29	1142.8	79.5	1634	24	AAS62516	cDNA sequence #303
30	1141.4	79.4	1356	25	AAD20745	Human recombinant
31	1141.4	79.4	1356	25	ABX79100	Mucin 1 (MUC-1) bi
32	1139.4	79.3	1412	13	AAQ25692	Sequence of the ch
33	1138.6	79.2	1347	21	AAZ60599	cDNA encoding a ra
34	1138.6	79.2	1590	24	ABK34976	Human cDNA encodin
35	1138.6	79.2	1640	24	ABK35183	Human cDNA encodin
36	1133.4	78.9	1599	24	ABK64550	Human benign prost
37	1133.4	78.9	1599	24	ABL62673	Colon adenocarcino
38	1133.4	78.9	1599	24	ABL65479	Lung cancer relate
39	1133.4	78.9	1599	24	ABL62294	Lung cancer relate
40	1131.8	78.8	1617	14	AAQ35099	Antibody D heavy c
41	1130.2	78.6	1449	20	AAX06951	Monoclonal antibod
42	1130.2	78.6	1449	20	AAX06952	Monoclonal antibod
c 43	1129.2	78.6	9182	24	ABK10574	Baculovirus expres
c 44	1127.8	78.5	1467	13	AAQ23570	Reshaped CAMPATH-1
c 45	1127.6	78.5	9182	24	ABL55051	Plasmid pTRABac/9F

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

```
RESULT 1
AAV35487
ID   AAV35487 standard; DNA; 1437 BP.
XX
AC   AAV35487;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 7B6 heavy chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1437
FT                   /*tag= a
FT                   /product= 7B6 heavy chain
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;  97WO-US19906.
XX
PR   08-NOV-1996;  96US-0746361.
XX
```

PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63763.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 4b; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 7B6 heavy chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   MAb's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 1437 BP; 329 A; 451 C; 387 G; 270 T; 0 other;

Query Match   100.0%; Score 1437; DB 19; Length 1437;
Best Local Similarity   100.0%; Pred. No. 1.1e-277;
Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAG 60

Qy   61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120

Qy   121 TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGGTCCGCCAGGCTCCA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGGTCCGCCAGGCTCCA 180

Qy   181 GGGAAGGGGCCGGAATGGGTAGGTTTCATTAGAAACAAACCGACGGTGGGACAACAGAA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGGAAGGGGCCGGAATGGGTAGGTTTCATTAGAAACAAACCGACGGTGGGACAACAGAA 240

Qy   241 TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAAGCATCGCC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAAGCATCGCC 300

Qy   301 TATCTGCAAATGAGCAGCCTGAAAATGCAGGACACGGCCCGTCTATTACTGTACTACATCC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TATCTGCAAATGAGCAGCCTGAAAATGCAGGACACGGCCCGTCTATTACTGTACTACATCC 360

Qy   361 TACATTTCAACATTGTCGGGGTGGTGTTGCTATGGCGTATGGAGGTTACTTCGAATTCTCGGGGCCAG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TACATTTCAACATTGTCGGGGTGGTGTTGCTATGGCGTATGGAGGTTACTTCGAATTCTCGGGGCCAG 420

Qy   421 GGCGCCCTGGTCACCGTGTCTCCTCAGCTAGCACCCAAGGGCCCATCCGTCTTCCCCCTGGCA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GGCGCCCTGGTCACCGTGTCTCCTCAGCTAGCACCCAAGGGCCCATCCGTCTTCCCCCTGGCA 480

Qy   481 CCCTCTCCAAGAGCACCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCCTCTCCAAGAGCACCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 540

Qy   541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 600

Qy   601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 660

Qy   661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 720

Qy   721 AAGGTGGACAAGAAAGCAGAGCCCAAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAGGTGGACAAGAAAGCAGAGCCCAAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 780

Qy   781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 840

Qy   841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 900

Qy   901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 960

Qy   961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 1020

Qy   1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1080

Qy   1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1140

Qy   1141 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1200

Qy   1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1260

Qy   1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1320

Qy   1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380

Qy   1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437

RESULT 2
AAS17245
ID   AAS17245 standard; DNA; 1437 BP.
XX
AC   AAS17245;
XX
DT   12-MAR-2002 (first entry)
XX
DE   DNA sequence of a primatised form of the heavy chain of 7B6 antibody.
XX

```
                    GenCore version 5.1.6
              Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     October  2, 2003, 13:05:20 ; Search time 2376.47 Seconds
                                          (without alignments)
                                          14696.420 Million cell updates/sec

Title:        US-09-758-173-7
Perfect score: 1437
Sequence:     1 ATGGGTTGGAGCCTCATCTT.......CCCTGTCTCCGGTAAATGA 1437

Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

Searched:     22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters:       45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    EST:*
          1:  em_estba:*
          2:  em_esthum:*
          3:  em_estin:*
          4:  em_estmu:*
          5:  em_estov:*
          6:  em_estpl:*
          7:  em_estro:*
          8:  em_htc:*
          9:  gb_esti:*
         10:  gb_est2:*
         11:  gb_htc:*
         12:  gb_est3:*
         13:  gb_est4:*
         14:  gb_est5:*
         15:  em_estfun:*
         16:  em_estom:*
         17:  em_gss_hum:*
         18:  em_gss_inv:*
         19:  em_gss_pln:*
         20:  em_gss_vrt:*
         21:  em_gss_fun:*
         22:  em_gss_mam:*
         23:  em_gss_mus:*
         24:  em_gss_pro:*
         25:  em_gss_rod:*
         26:  em_gss_phg:*
         27:  em_gss_vrl:*
         28:  gb_gss1:*
         29:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
Result       %    Query
No.   Score  Match Query Length DB ID      Description
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c  1  948.2  66.0  1201  1201  13  BX377695  BX377695 BX377695
c  2  929.6  64.7  1142  1142  13  BX414495  BX414495 BX414495
c  3  902    62.8  1020  1020  12  BQ062878  BQ062878 AGENCOURT
c  4  899.2  62.6  1045  1045  13  BX337477  BX337477 BX337477
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c  5  894.8  62.3  1149  13  BX381020  BX381020
c  6  892.6  62.1  1201  13  BX377803  BX377803
c  7  891.2  61.9  1201  13  BX439438  BX439438
c  8  889.8  61.9  902   13  BU146962  AGENCOURT
c  9  875.8  60.9  1013  13  BX360518  BX360518
c 10  867.6  60.4  1200  13  BX415883  BX415883
  11  864    60.1  947   13  BQ709771  AGENCOURT
c 12  850.4  59.2  958   13  BQ706140  AGENCOURT
  13  849.2  59.1  1093  13  BX428863  BX428863
  14  842.4  58.6  926   10  BG755166  602711488
c 15  837.4  58.3  988   13  BQ708857  AGENCOURT
  16  832    57.9  1096  13  BX415920  BX415920
c 17  831.8  57.9  1201  13  BX338493  BX338493
  18  830.8  57.8  901   12  BM007892  603617577
c 19  830.6  57.8  985   13  BX457369  BX457369
  20  829.4  57.7  1201  13  BX417147  BX417147
  21  824.4  57.4  1029  12  BQ063185  AGENCOURT
  22  823.8  57.3  918   13  BQ708022  AGENCOURT
c 23  823.2  57.3  1019  13  BX325650  BX325650
  24  822.8  57.3  887   13  BQ711255  AGENCOURT
  25  819    57.0  995   12  BM914540  AGENCOURT
c 26  818    56.9  1015  13  BX367600  BX367600
c 27  817.8  56.9  980   13  BX325701  BX325701
  28  811.8  56.5  889   13  BX346909  BX346909
c 29  811    56.4  1147  13  BX360330  BX360330
c 30  809    56.3  1009  13  BX456658  BX456658
  31  808.8  56.3  881   13  BQ711291  AGENCOURT
c 32  807.4  56.2  1200  13  BX456326  BX456326
  33  804    55.9  853   13  BX388631  BX388631
  34  801.6  55.8  862   13  BX450248  BX450248
  35  800.2  55.7  1031  13  BQ064886  AGENCOURT
  36  799.4  55.6  852   13  BX450232  BX450232
c 37  798.4  55.6  1004  13  BX432300  BX432300
  38  797.4  55.5  936   13  BQ711727  AGENCOURT
  39  796    55.4  940   13  BQ705928  AGENCOURT
c 40  795.6  55.4  1070  13  BX397632  BX397632
c 41  795.2  55.3  1152  13  BX339318  BX339318
c 42  794.2  55.3  1151  13  BX378450  BX378450
  43  792.2  55.1  885   13  BX408117  BX408117
c 44  791.2  55.1  1201  13  BX396322  BX396322
c 45  788.8  54.9  1201  13  BX439176  BX439176
```

ALIGNMENTS

RESULT 1
BX377695/c

```
LOCUS       BX377695                1201 bp    mRNA       linear    EST 08-MAY-2003
DEFINITION  BX377695 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI009YJ10 3-PRIME, mRNA sequence.
ACCESSION   BX377695
VERSION     BX377695.1  GI:30439018
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI009DE05NP1&cluster=7198.r. Contact :
            Feng Liang Email: fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
```

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Db    346 TCAGCCTGACCTGGTCAAGGCTTTTATCCCAGCGACCATCGCCGTTGGAGTGGGAGA 287
          ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Qy   1241 GCAATGGGACCGGAGAACAACTACAAGACCACGCACCGCCTCCCGTTGCTTGGACTCCGACGGCT 1300
          |||||||||||||||||||||   :||||||||||||||||   ||:|||||||||||||||||||
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Qy   1301 CCTTCTTCCTCCTACAGCAAGTCACCTGTGACAAGAGAGCAGGTGGCAGCAGGGGAACGTCT 1360
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Db    226 CCTTCTTCCTCCTACAGCAAGTCACCTGTGACAAGAGAGCAGGTGGCAGCAGGGGAACGTCT 167

Qy   1361 TCTCATGCTCCGTGATGCATGAGGCTCTGCACACACACGCAGAGAGCCTCTCCC 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    166 TCTCATGCTCCGTGATGCATGAGGCTCTGCACACACACGCAGAGAGCCTTCTCCT 107

Qy   1421 TGTCTCCGGGTAAATGA 1437
          |||||||||||||||||
Db    106 TTTCTCCGGGTAAATGA 90
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RESULT 2
BX414495/c
LOCUS          BX414495        1142 bp    mRNA    linear    EST 13-MAY-2003
DEFINITION     BX414495 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001Y113
               3-PRIME, mRNA sequence.
ACCESSION      BX414495
VERSION        BX414495.1    GI:30637021
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1142)
AUTHORS        Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished
COMMENT        Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 7198.r For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0CAP001AE07NP1&cluster=7198.r. Contact :
               Feng Liang Email: fliang@lifetech.com URL :
               http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0CAP001AE07NP1.
FEATURES       Location/Qualifiers
   source      1..1142
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="CS0CAP001Y113"
               /tissue_type="THYMUS"
               /clone_lib="Homo sapiens THYMUS"
               /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
               with a NotI-oligo(dT) primer. Five prime end enriched,
               double-strand cDNA was digested with Not I and cloned into
               the Not I and EcoRV sites of the pCMVSPORT 6 vector.
               Library was not normalized."
BASE COUNT     193 a    290 c    381 g    251 t    27 others
ORIGIN
```

```
Query Match      64.7%;    Score 929.6;  DB 13;  Length 1142;
Best Local Similarity   98.2%;   Pred. No. 3.6e-205;
Matches  952;   Conservative   6;  Mismatches   9;   Indels   2;   Gaps   2;

Qy    469 TTCCCCCTGGACACCCTCCTCCAAGAGACCACCTGTGGGGCACAGCCGCCTGGGCTGCCTG 528
          ||||| |||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   1078 TTTCCCCTTGGACCCCTCCTCAAAGAGMACTTCTGGGGG-AMAGCSGCCCTGCGCTGCCTG 1020
Qy    529 GTCAAGGACTACTTCCCGAACCGGTGACCGGTGTCGTGGAACTCATGCTGGCCGCCTGACCAGC 588
```